

SEARCH REQUEST FORM

Scientific and Technical Information Center

57382

Requester's Full Name

J. Hines CM-2 2

Examiner # : _____

Date: 1/3/02

Art Unit:

1645

Phone Number 305-0487

Serial Number:

091335.581

Mail Box and Bldg/Room Location: CM 9A71C Results Format Preferred (circle): PAPER DISK E-MAIL

7E/2

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention:

Peptide for toxic Shock Syndrome

Inventors (please provide full names):

Jason D. Bannan, Kumar Visvanathan

JOHN B. ZABISKIE

Earliest Priority Filing Date:

6/18/99

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search the inventor and

Please search SEQ ID NO: 3 and 34

Thanks

Point of Contact:

Mona Smith

Technical Info. Specialist

CM 12C14 Tel: 308-3278

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____

NA Sequence (#) _____

STN _____

AA Sequence (#) _____

Dialog _____

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=> fil hcaplu

FILE 'HCAPLUS' ENTERED AT 11:26:24 ON 03 JAN 2002

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FILE COVERS 1907 - 3 Jan 2002 VOL 136 ISS 1

FILE LAST UPDATED: 2 Jan 2002 (20020102/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of all substance data from the REGISTRY file. Enter HELP FIRST for more information.

HCAplus now provides online access to patents and literature covered in CA from 1907 to the present. Bibliographic information and abstracts were added in 2001 for over 3.8 million records from 1907-1966.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

=> d stat que

L1 14 SEA FILE=HCAPLUS ("BANNAN J D"/AU OR "BANNAN JASON"/AU OR
"BANNAN JASON D"/AU OR "BANNAN JASON D"/IN OR "BANNAN JASON
DAVID"/AU)
L2 19 SEA FILE=HCAPLUS ("VISVANATHAN K"/AU OR "VISVANATHAN K S"/AU
OR "VISVANATHAN KANNA V"/AU OR "VISVANATHAN KUMAR"/AU OR
"VISVANATHAN KUMAR"/IN)
L3 73 SEA FILE=HCAPLUS ("ZABRISKIE J"/AU OR "ZABRISKIE J B"/AU) OR
("ZABRISKIE JOHN"/AU OR "ZABRISKIE JOHN B"/AU OR "ZABRISKIE
JOHN B"/IN)
L4 2 SEA FILE=HCAPLUS L1 AND L2 AND L3

=> d ibib abs hitrn l4 1-2

L4 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:76096 HCAPLUS

DOCUMENT NUMBER: 134:250923

TITLE: Inhibition of bacterial superantigens by peptides and
antibodies

AUTHOR(S): Visvanathan, Kumar; Charles, Alain;

THIS PAGE BLANK (USPTO)

Bannan, Jason; Pugach, Pavel; Kashfi, Khosrow; Zabriskie, John B.
CORPORATE SOURCE: Laboratory of Clinical Microbiology and Immunology,
Rockefeller University, New York, NY, 10021, USA
SOURCE: Infect. Immun. (2001), 69(2), 875-884
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The pyrogenic exotoxins of group A streptococci and staphylococcal enterotoxins are a family of structurally related superantigens with similar biol. activity. Two distinct areas have been identified which have a highly conserved amino acid homol. in all of the toxin families. A no. of peptides were constructed from these regions, some of which were concatenated and polymd. to enhance their immunogenicity in animals. Antibodies prepd. against these polymd. peptides were used to serol. identify the majority of the superantigen toxins, block the biol. activities of the superantigens, and protect an exptl. animal model against shock. In addn. certain peptides were able per se to block up to 90% of the proliferative responses induced by the toxins. The peptide also proved protective in a septic shock model in mice. Binding expts. indicate that the peptide binds tightly to the major histocompatibility complex class II mol., thus preventing binding and hence activation of the superantigen. The selective and rapid binding of the peptide to the major histocompatibility complex class II mol. may lead to a novel therapeutic modality in treatment of superantigen-mediated diseases.

REFERENCE COUNT: 23

REFERENCE(S): (1) Arad, G; Nat Med 2000, V6, P414 HCAPLUS
(2) Bannan, J; Adv Exp Med Biol 1997, V418, P903 HCAPLUS
(4) Blank, C; Eur J Immunol 1997, V27(4), P825 HCAPLUS
(5) Eriksson, A; Microb Pathog 1998, V25, P279 HCAPLUS
(6) Fridkis-Hareli, M; J Immunol 1998, V160(9), P4386 HCAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:241505 HCAPLUS

DOCUMENT NUMBER: 132:290233

TITLE: Sequences of peptides derived from staphylococcal and streptococcal toxins, and applications thereof in diagnosing and treating toxic shock syndrome and septic shock

INVENTOR(S): **Bannan, Jason D.; Visvanathan, Kumar; Zabriskie, John B.**

PATENT ASSIGNEE(S): Rockefeller University, USA

SOURCE: PCT Int. Appl., 115 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.

KIND DATE

APPLICATION NO. DATE

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WO 2000020598      A1      20000413      WO 1999-US22180  19990924
W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
    CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
    IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD,
    MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
    SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY,
    KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
    DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
    CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9960597          A1      20000426      AU 1999-60597      19990924
EP 1127132          A1      20010829      EP 1999-970123    19990924
R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
    IE, SI, LT, LV, FI, RO
PRIORITY APPLN. INFO.:      US 1998-168303  A  19981007
                              US 1999-335581  A  19990618
                              WO 1999-US22180  W  19990924

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OTHER SOURCE(S): MARPAT 132:290233

AB This invention relates to amino acid sequences of peptides useful for providing protection against, or reducing the severity of, toxic shock and septic shock resulting from bacterial infections. More particularly, the invention provides peptides derived from consensus sequences of the family of staphylococcal and streptococcal toxins, and may be polymeric and/or carrier-conjugates thereof. The invention also relates to serum antibodies induced by the peptides and/or carrier-conjugates and their use to prevent, treat, or protect against the toxic effects of most, if not all, of the staphylococcal and streptococcal toxins. Antibodies may be induced by administration of a pharmaceutical compn. and/or vaccine contg. a peptide of the invention. The invention also relates to diagnostic assays and kits to detect the presence of staphylococcal and streptococcal toxins, or antibodies thereto.

REFERENCE COUNT: 5

REFERENCE(S): (1) Bannan, J; WO 9845325 A 1998 HCAPLUS
 (2) Bannan, J; INFECTIOUS DISEASE CLINICS OF NORTH
 AMERICA 1999, V13(2), P387 MEDLINE
 (3) National Jewish Center For Immunology And
 Respiratory Medicine; WO 9636366 A 1996 HCAPLUS
 (4) Schlievert, P; WO 9640930 A 1996 HCAPLUS
 (5) Terman, D; WO 9110680 A 1991 HCAPLUS

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:46:42 : Search time 40.75 Seconds
(without alignments)
6.627 Million cell updates/sec

Title: US-09-335-581A-34
Perfect score: 71
Sequence: 1 CMYGVTLHEGN 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfilea1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	14	4 US-08-896-933-13	Sequence 13, Appl
2	64	90.1	12	3 US-08-838-413A-3	Sequence 3, Appl
3	64	90.1	12	3 US-08-838-413A-11	Sequence 11, Appl
4	64	90.1	14	3 US-08-838-413A-5	Sequence 5, Appl
5	64	90.1	14	4 US-08-896-933-5	Sequence 5, Appl
6	64	90.1	36	3 US-08-838-413A-7	Sequence 7, Appl
7	64	90.1	38	3 US-08-838-413A-8	Sequence 8, Appl
8	64	90.1	238	4 US-08-896-933-28	Sequence 28, Appl
9	64	90.1	239	4 US-08-896-933-27	Sequence 27, Appl
10	62	87.3	12	3 US-08-838-413A-9	Sequence 9, Appl
11	62	87.3	12	3 US-08-838-413A-13	Sequence 13, Appl
12	62	87.3	14	4 US-08-896-933-1	Sequence 1, Appl
13	62	87.3	14	4 US-08-896-933-9	Sequence 9, Appl
14	62	87.3	23	1 US-08-230-378-5	Sequence 5, Appl
15	62	87.3	23	1 US-08-696-012-5	Sequence 5, Appl
16	62	87.3	226	4 US-08-896-933-24	Sequence 24, Appl
17	62	87.3	232	4 US-08-896-933-23	Sequence 23, Appl
18	62	87.3	233	1 US-08-446-918A-4	Sequence 4, Appl
19	62	87.3	257	3 US-08-580-806-4	Sequence 4, Appl
20	62	87.3	257	3 US-08-486-099-112	Sequence 112, App
21	62	87.3	257	3 US-08-486-099-113	Sequence 113, App
22	62	87.3	257	3 US-08-360-107A-122	Sequence 122, App
23	62	87.3	257	3 US-08-360-107A-123	Sequence 123, App
24	62	87.3	257	3 US-08-484-223B-112	Sequence 112, App
25	62	87.3	257	3 US-08-484-223B-113	Sequence 113, App
26	62	87.3	257	3 US-08-919-597-112	Sequence 112, App
27	62	87.3	257	3 US-08-919-597-113	Sequence 113, App

28	62	87.3	257	3	US-08-475-668A-112	Sequence 112, App
29	62	87.3	257	3	US-08-475-668A-113	Sequence 113, App
30	62	87.3	257	3	US-08-485-551A-112	Sequence 112, App
31	62	87.3	257	3	US-08-485-551A-113	Sequence 113, App
32	62	87.3	257	3	US-08-471-913A-112	Sequence 112, App
33	62	87.3	257	3	US-08-471-913A-113	Sequence 113, App
34	62	87.3	257	4	US-08-485-264A-112	Sequence 112, App
35	62	87.3	257	4	US-08-485-264A-113	Sequence 113, App
36	61	85.9	220	4	US-08-896-933-20	Sequence 20, Appl
37	60	84.5	12	3	US-08-838-413A-15	Sequence 15, Appl
38	60	84.5	14	4	US-08-896-933-11	Sequence 11, Appl
39	60	84.5	221	4	US-08-896-933-29	Sequence 29, Appl
40	59	83.1	12	3	US-08-838-413A-10	Sequence 10, Appl
41	59	83.1	13	4	US-08-896-933-3	Sequence 3, Appl
42	59	83.1	239	4	US-08-896-933-26	Sequence 26, Appl
43	59	83.1	235	1	US-08-446-918A-2	Sequence 2, Appl
44	59	83.1	255	2	US-08-580-806-2	Sequence 2, Appl
45	58	81.7	12	3	US-08-838-413A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-896-933-13
Sequence 13, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Other
FEATURE:
OTHER INFORMATION: Consensus sequences derived from staphylococcus
US-08-896-933-13
Query Match 100.0%; Score 71; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. NO. 4.7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CMYGVTLHEGN 12
Db 1 CMYGVTLHEGN 12
RESULT 2
US-08-838-413A-3
Sequence 3, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

PAT 6,122,135
PAT 6,126,945
10/3/00

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-3

Query Match 90.1%; Score 64; DB 3; Length 12;
Best Local Similarity 91.7%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
|||||
Db 1 CMYGVTEHEGN 12

RESULT 3
US-08-838-413A-11
Sequence 11, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-11

Query Match 90.1%; Score 64; DB 3; Length 12;
Best Local Similarity 83.3%; Pred. No. 7e-05;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
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Db 1 CMYGVTLHEGN 12

RESULT 4
US-08-838-413A-5
Sequence 5, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-5

Query Match 90.1%; Score 64; DB 3; Length 14;
Best Local Similarity 91.7%; Pred. No. 7.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
| | | | | | | | | |
Db 1 CMYGGVTEHEGN 12

RESULT 5

US-08-896-933-5

Sequence 5, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

FILE REFERENCE: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

CURRENT FILING DATE: 1997-07-18

EARLIER APPLICATION NUMBER: 08/252,978

EARLIER FILING DATE: 1994-06-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 14

TYPE: PRT

ORGANISM: Staphylococcus aureas

US-08-896-933-5

Query Match 90.1%; Score 64; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.1e-05;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
| | | | | | | | | |
Db 1 CMYGGITKHEGN 12

RESULT 6

US-08-838-413A-7

Sequence 7, Application US/08838413A

Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)758-4800

TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-7

Query Match 90.1%; Score 64; DB 3; Length 36;
Best Local Similarity 91.7%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
| | | | | | | | | |
Db 1 CMYGGVTEHEGN 12

RESULT 7

US-08-838-413A-8

Sequence 8, Application US/08838413A

Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)758-4800

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 38

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-8

Query Match 90.1%; Score 64; DB 3; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
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Db 1 CMYGGVTEHGN 12

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RESULT 8
US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-28

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Query Match
Best Local Similarity 90.1%; Score 64; DB 4; Length 238;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CMYGGVTEHGN 12
Db 109 CMYGGITKHEGN 120

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RESULT 9
US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-27

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Query Match
Best Local Similarity 90.1%; Score 64; DB 4; Length 239;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CMYGGVTEHGN 12
Db 110 CMYGGITKHEGN 121

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RESULT 10
US-08-838-413A-9
; Sequence 9, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES USEFUL FOR

```

```

; TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,413A
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRIS, MARY J.
; REGISTRATION NUMBER: 34,398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
US-08-838-413A-9

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Query Match
Best Local Similarity 87.3%; Score 62; DB 3; Length 12;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CMYGGVTEHGN 12
Db 1 CMYGGVTEHGN 12

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RESULT 11
US-08-838-413A-13
; Sequence 13, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES USEFUL FOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,413A
; FILING DATE: 07-APR-1997

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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-13

Query Match 87.3%; Score 62; DB 3; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.00013;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
Db 1 CMYGVTLHDNN 12

RESULT 12
US-08-896-933-1
Sequence 1, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 14
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-896-933-1

Query Match 87.3%; Score 62; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 0.00015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
Db 1 CMYGVTLHDNN 12

RESULT 13
US-08-896-933-9
Sequence 9, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18

EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 14
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-896-933-9

Query Match 87.3%; Score 62; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 0.00015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
Db 1 CMYGVTLHDNN 12

RESULT 14
US-08-220-378-5
Sequence 5, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI26.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-5

Query Match 87.3%; Score 62; DB 1; Length 23;
Best Local Similarity 83.3%; Pred. No. 0.00026;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
Db 1 CMYGVTLHDNN 12

Db 5 CMYGVTLHDNN 16

RESULT 15

US-08-696-012-5

; Sequence 5, Application US/08696012

; Patent No. 5859207

GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.

APPLICANT: Pontzer, Carol H.

APPLICANT: Griggs, Nathan D.

TITLE OF INVENTION: Superantigen Agonist and Antagonist

TITLE OF INVENTION: Peptides

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/696,012

FILING DATE: 12-AUG-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/220,378

FILING DATE: 29-MAR-1994

APPLICATION NUMBER: US 07/941,497

FILING DATE: 08-SEP-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UF126.C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-696-012-5

Query Match 87.3%; Score 62; DB 2; Length 23;

Best Local Similarity 83.3%; Pred. No. 0.00026;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHESN 12

Db 5 CMYGVTLHDNN 16

Search completed: January 2, 2002, 20:46:42
Job time: 11488 sec

35

Although the foregoing invention has been described in detail for purposes of clarity of understanding, certain modifications may be practiced within the scope of the appended claims. While the above findings apply to an experimental animal model, it should be recognized that the tumor used herein is an excellent model of human cancer. Therapeutic success in the canine model with PACC system (described in a series of patent applications, the latest of which is identified as Ser. No. 331,095), the forerunner of the present invention, was transferred to humans in which objective tumor regressions were obtained in four of the first five consecutive patients treated. Thus, the data given herein for rabbits with carcinoma is expected to be predictive of success when the compositions are applied to humans with spontaneous tumors as well.

In the method of treating cancer in a patient utilizing a single step of administering Staphylococcal enterotoxins or enterotoxin fragments, a tumoricidally effective amount of the enterotoxin or enterotoxin fragment is between 0.5 μ g (enterotoxin) per kg (body weight) and 150 μ g (enterotoxin) per kg (body weight). This tumoricidally effective amount applies to the enterotoxins which are chemically derivatized.

We claim:

1. A method of treating a subject having a tumor comprising administering to the subject a tumoricidally effective amount of a toxin selected from the group consisting of a staphylococcal enterotoxin and a streptococcal pyrogenic exotoxin.
2. The method of claim 1, wherein the toxin is a staphylococcal enterotoxin.
3. The method of claim 2 wherein the staphylococcal enterotoxin is selected from the group consisting of enterotoxin A, B, C, D, E, and F.
4. The method of claim 2 wherein the staphylococcal enterotoxin is a biologically active fragment of an enterotoxin.
5. The method of claim 2 wherein the staphylococcal enterotoxin has been chemically derivatized to minimize toxicity while retaining tumoricidal activity.

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6. The method of claim 1 wherein the toxin is administered by intravenous inoculation.

7. The method of claim 1 wherein the tumor is a carcinoma.

8. A method of treating a patient having a tumor comprising administering to the patient a tumoricidally effective amount of a toxin selected from the group consisting of a staphylococcal enterotoxin and a streptococcal pyrogenic exotoxin.

9. The method of claim 8 wherein the toxin is a staphylococcal enterotoxin.

10. The method of claim 9 wherein the staphylococcal enterotoxin is selected from the group consisting of enterotoxin A, B, C, D, E, and F.

11. The method of claim 10 wherein the staphylococcal enterotoxin is enterotoxin B.

12. The method of claim 8 wherein the tumor is a carcinoma.

13. The method of claim 9 wherein the staphylococcal enterotoxin is a biologically active fragment of an enterotoxin.

14. The method of claim 9 wherein the staphylococcal enterotoxin has been chemically derivatized to minimize toxicity while retaining tumoricidal activity.

15. The method of claim 9 wherein the chemical derivatization is carboxymethylation.

16. The method of claim 15 wherein the carboxymethylated toxin comprises carboxymethylated enterotoxin B.

17. The method of claim 11 wherein the enterotoxin B has been purified to remove alpha hemolysin.

18. The method of claim 11 wherein the enterotoxin B contains no more than 0.1 microgram endotoxin per milligram enterotoxin B.

19. The method of claim 8 wherein the toxin is administered by intravenous inoculation.

* * * * *

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61

26. The method of claim 25, wherein the in vitro culture includes interleukin 2.

27. The method of claim 15 or 16, wherein the superantigen is expressed on the surface of the transfected cells.

28. The method of claim 15 or 16, wherein the transfected cells expresses MHC class II molecules.

29. A method for increasing antitumor immunity against a tumor in a mammal, comprising contacting tumor cells that are transfected with nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen with the immune system of said mammal,

wherein expression of the superantigen or polypeptide by the transfected cells induces T cell proliferation and increases said antitumor immunity.

30. A method for increasing antitumor immunity against a tumor in a mammal, comprising contacting accessory cells, immunocytes or fibroblasts that are transfected with nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen with the immune system of said mammal,

wherein expression of the superantigen or polypeptide by the transfected cells induces T cell proliferation and increases said antitumor immunity.

31. The method of claim 29 or 30, wherein the mammal is a human.

32. The method of claim 29 or 30, wherein the superantigen is selected from the group consisting of a Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, toxic shock syndrome toxin, a mycoplasma antigen, a mycobacteria antigen, a minor lymphocyte stimulating antigen, a heat shock protein, a stress peptide, and a derivative thereof.

33. The method of claim 29 or 30, wherein the tumor cells, accessory cells, immunocytes or fibroblasts are transfected in vivo.

34. The method of claim 29 or 30, wherein the tumor cells, accessory cells, immunocytes or fibroblasts are transfected in vitro.

35. The method of claim 34, wherein the transfected cells are tumor cells, and the contacting comprises administering the transfected tumor cells to the mammal.

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36. The method of claim 29 or 30, wherein the contacting comprises administering the transfected cells to the mammal.

37. The method of claim 29 or 30, wherein the contacting comprises:

(i) incubating the transfected cells ex vivo with an immunocyte population to tumoricidally activate the population, and

(ii) administering the activated population to the mammal.

38. The method of claim 37, wherein the immunocyte population being activated comprises T cells.

39. The method of claim 37, wherein the activated immunocytes are expanded by in vitro culture prior to their administration.

40. The method of claim 39, wherein the in vitro culture includes interleukin 2.

41. The method of claim 29 or 30, wherein the superantigen is expressed on the surface of the transfected cells.

42. The method of claim 29 or 30, wherein the transfected cells express MHC class II molecules.

43. A method for treating cancer in a tumor-bearing host, comprising administering a nucleic acid encoding a superantigen to said tumor in vivo to transfect tumor cells, wherein expression of said superantigen induces a tumoricidal immune response, thereby treating said cancer.

44. A method of killing tumor cells in a mammal, comprising administering a nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen to said tumor in vivo to transfect tumor cells, wherein expression of the superantigen or polypeptide produces a tumoricidal immune response resulting in the killing of said tumor cells.

45. A method for increasing antitumor immunity against a tumor in a tumor-bearing mammal, comprising administering a nucleic acid encoding a superantigen or biologically active polypeptide of a superantigen to said tumor in vivo to transfect tumor cells, wherein expression of the superantigen or polypeptide induces T cell proliferation and increases said antitumor immunity.

46. The method of any of claims 43-45 wherein said mammal or host is a human.

* * * * *

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 17:59:24 ; Search time 77.31 Seconds
(without alignments)
11.498 Million cell updates/sec

Title: US-09-335-581A-3

Perfect score: 72

Sequence: 1 CMYCGVTEHEGN 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	12	19	AAW72422
2	72	100.0	12	21	AAV97838
3	72	100.0	12	22	AAV72176
4	72	100.0	14	19	AAW72424
5	72	100.0	14	21	AAV97840
6	72	100.0	14	22	AAV72178
7	72	100.0	36	19	AAW72426
8	72	100.0	36	21	AAV97842
9	72	100.0	36	22	AAV72180
10	72	100.0	38	19	AAW72427
11	72	100.0	38	21	AAV97843

12	72	100.0	38	22	AAV72181	peptide #6348, der
13	67	93.1	12	21	AAV97845	Staphylococcus aur
14	67	93.1	12	21	AAV97846	Staphylococcus aur
15	67	93.1	12	22	AAV72183	Peptide from regio
16	67	93.1	12	22	AAV72184	Peptide from regio
17	67	93.1	238	12	AAV72180	Staphylococcus ent
18	67	93.1	238	14	AAV5016	Staphylococcus ent
19	67	93.1	238	12	AAV72181	Staphylococcus ent
20	67	93.1	239	12	AAV72182	Staphylococcus ent
21	67	93.1	239	12	AAV72183	Staphylococcus ent
22	67	93.1	239	14	AAV5014	Staphylococcus ent
23	67	93.1	239	14	AAV5015	Staphylococcus ent
24	67	93.1	239	19	AAV5016	Synthetic SEB prot
25	67	93.1	239	20	AAV6254	Staphylococcus gro
26	67	93.1	239	20	AAV6255	Staphylococcus gro
27	67	93.1	239	20	AAV6256	Staphylococcus gro
28	67	93.1	239	20	AAV6257	Staphylococcus gro
29	67	93.1	239	20	AAV6258	Staphylococcus gro
30	67	93.1	239	20	AAV6259	Staphylococcus gro
31	67	93.1	239	20	AAV6260	Staphylococcus gro
32	67	93.1	239	21	AAV6261	Staphylococcus gro
33	67	93.1	239	21	AAV6262	Staphylococcus gro
34	67	93.1	239	22	AAV6263	Staphylococcus gro
35	67	93.1	239	22	AAV6264	Staphylococcus gro
36	67	93.1	240	21	AAV54465	Mutant Staphylococ
37	67	93.1	255	18	AAV6737	Staphylococcus ent
38	67	93.1	265	21	AAV70104	Staphylococcus ent
39	67	93.1	265	21	AAV70105	Mutant Staphylococ
40	67	93.1	266	21	AAV92319	Plant-optimized mu
41	67	93.1	266	21	AAV70108	Staphylococcus ent
42	67	93.1	266	21	AAV54464	Amino acid sequenc
43	63	87.5	12	21	AAV7850	Group A streptococ
44	63	87.5	12	22	AAV72188	Peptide from regio
45	63	87.5	221	12	AAV7209	Streptococcus pyro

ALIGNMENTS

RESULT 1
ID AAW72422 standard; peptide: 12 AA.
XX AAW72422;
AC 22-DEC-1998 (first entry)
DT 22-DEC-1998 (first entry)
XX Peptide #1 for reducing symptoms of toxic shock syndrome.
DE Toxic shock syndrome; immunogenic response; bacterial infection;
KW Streptococcus enterotoxin; Streptococcus pyrogenic toxin; antibody;
KW autoimmune disease.
XX Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
XX WO9845325-A1.
XX 15-OCT-1998.
XX 01-APR-1998; 98WO-US06663.
XX 07-APR-1997; 97US-0838413.
XX (UVRQ) UNIV ROCHEFELT.
XX Bannan JD, Zabitskie JB;
XX WPI; 1998-568335/48.
XX New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic

PT	shock and autoimmune diseases
XX	
PS	Claim 4; Page 53; 69pp; English.
XX	
CC	The present invention describes peptides having consensus sequences #1
CC	or #2, optionally as part of a larger molecule of size at least 6-8 kd
CC	where consensus sequence #1 and #2 are: X23X26YGGX17X23X4X5N #1,
CC	K6X7X8YX10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
CC	X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC	or are absent; X27 = L or Y; all other X may be any aa. The peptides
CC	can be used to generate serum antibodies (Ab) that bind at least one
CC	staphylococcal enterotoxin (SE) or streptococcal endotoxin (SED). Ab
CC	are used: (1) for diagnostic detection of SPEA or SEA, SEB and SED, in
CC	usual immunoassays; (11) to inhibit blastogenesis of human mononuclear
CC	cells in presence of these toxins (i.e. to protect against or alleviate
CC	toxic shock or autoimmune disease associated with bacterial infections
CC	and (111) for passive immunisation against effects of the toxins. The
CC	peptides generate Ab that are cross-reactive with toxins from a variety
CC	of bacteria. The present sequence represents a specifically claimed
CC	example of a peptide of the present invention.
XX	
SQ	Sequence 12 AA:
QY	1 CMYGVTEHGN 12
DT	1 cmygvtehgn 12
QY	100.0%; Score 72; DB 19; Length 12;
DT	Best Local Similarity 100.0%; Pred. No. 3.5e-06;
DT	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps
RESULT 2	
AA97838	
ID	AA97838 standard; peptide; 12 AA.
AC	AA97838;
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6343.
XX	
KM	Pyrogenic exotoxin; enterotoxin; streptococcal infection;
KM	staphylococcal infection; septic shock; toxic shock; vaccine;
XX	antibody.
OS	Synthetic.
OS	Staphylococcus aureus.
OS	Streptococcus sp. 'Group A'.
PN	MO200020598-A1.
PD	13-APR-2000.
XX	
PF	24-SEP-1999; 99WO-US22180.
XX	
PR	07-OCT-1998; 98US-0168303.
PR	18-JUN-1999; 99US-0335581.
XX	
PA	(UYRO) UNIV ROCKEFELLER.
XX	
PI	Bannan JD, Visvanathan K, Zabriskie JB;
DR	WPI: 2000-303782/26.
XX	
PT	Peptides useful for preventing and reducing the symptoms of toxic shock
PT	syndrome and septic shock from staphylococcal and streptococcal
XX	infections -
PS	Claim 4; Page 88; 115pp; English.
XX	
XX	The invention relates to novel peptides (AA97838-Y97843) comprising a

consensus amino acid sequence derived from two conserved regions (regions 1 and 2) of *Staphylococcus aureus* enterotoxins and streptococcal pyrogenic toxins. Consensus region 1a (a preferred consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N (AA597863) and consensus region 2a (a preferred consensus region 2) has the sequence K-X6-X7-X8-X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y (AA597864), where: X1, X8, X13 and X24 are each independently selected from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16, X17, X18, X19, X20, X21, X22 and X23 are each independently selected from the group consisting of any amino acid; X3, X5 and X26 are each independently selected from the group consisting of any amino acid and of no amino acid; X27 is either L or Y.

The invention also relates to serum antibodies induced by the peptides which provide protection against, or reduce the severity of toxic shock and septic shock caused by the staphylococcal and streptococcal pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and the enterotoxins of *Staphylococcus aureus* (which are also pyrogenic exotoxins) constitute a family of structurally related toxins which share similar biological activities. They stimulate CD4⁺, CD8⁺ and gamma-delta⁺ T-cells by binding the beta-chain variable region (V-beta) elements on the lateral face of the T-cell receptor (TCR) while simultaneously binding the lateral face of the class II major histocompatibility complex (MHC) of antigen presenting cells. This causes aberrant proliferation of T-cells, which stimulates other components of the immune system, causing injury to the host. The peptides are used to prevent, treat or protect against toxic shock and septic shock resulting from bacterial infections in mammals, particularly humans. The peptides are used for inducing serum antibodies that bind at least one staphylococcal enterotoxin or streptococcal exotoxin and both the peptides and antibodies can be used in diagnostic assays to aid in the diagnosis of disease related to the presence of bacterial toxins. Nucleic acids encoding a peptide of the invention can be used for the production of the peptides for diagnostic reagents, as vaccines and for therapies for pyrogenic exotoxin related diseases. Vectors expressing high levels of the peptides can be used in immunotherapy and immunoprophylaxis when expressed in humans. The antibodies are used for passive immunisation therapy to prevent or increase resistance to toxic shock syndrome or septic shock and to ameliorate the effects of conditions associated with the presence of staphylococcal or streptococcal pyrogenic toxins. The amino acid sequences of the peptides are sufficiently common that they can be used for eliciting antibodies which are cross-reactive with toxins derived from various bacteria. Sequences AA597838-Y978343 represent the synthetic peptides based on consensus consensus regions 1 and 2 of *Staphylococcus aureus* and Group A streptococcal pyrogenic toxins. These peptides can be administered to a mammal to raise serum antibodies for protection against or amelioration of toxic or septic shock.

Sequence 12 AA:

Query Match 100.0%; Score 72; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 3,5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHGN 12
|||||
Db 1 cmvgvtehegn 12

RESULT 3
AA572176
ID AA572176 standard; peptide: 12 AA.
XX
XX AA572176:
DT 24-APR-2001 (first entry)
DE Peptide #6343, derived from streptococcal and staphylococcal toxins.
XX
XX Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
NM staphylococcal enterotoxin; human immunodeficiency virus; T cell;

KM streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.
 XX Streptococcus sp.
 OS Staphylococcus sp.
 XX WO200078790-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000WO-US16680.
 XX
 PR 18-JUN-1999; 99US-0336627.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 XX
 PI Visvanathan K, Zabriskie JB;
 DR WPI: 2001-080820/09.
 XX
 PT Providing protection against, and reducing the severity of, human
 PT immunodeficiency virus infections and associated deleterious effects,
 PT using peptides from homologous sequences of staphylococcal and
 PT streptococcal toxins
 XX
 PS Claim 5; Page 38; 76pp; English.
 XX
 CC The present sequence is peptide #6343, derived from region 1 of
 CC the homologous sequences of staphylococcal enterotoxin and
 CC streptococcal pyrogenic exotoxin.
 CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
 CC against the peptide are useful for inhibiting blastogenesis of
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against
 CC the deleterious effects of HIV. The peptide is also used to ameliorate
 CC the effects of autoimmune diseases associated with the presence of HIV.
 CC The Ab is used for passively immunising a mammal against the deleterious
 CC effects of HIV.
 XX
 SQ Sequence 12 AA:
 Query Match 100.0%; Score 72; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CMYGVTEHEGN 12
 Db | | | | | | | | | | | |
 1 cmgygtehegn 12
 RESULT 4
 AAW72424
 ID AAW72424 standard; peptide: 14 AA.
 XX
 AC AAW72424;
 XX
 DT 22-DEC-1998 (first entry)
 XX
 DE Peptide #3 for reducing symptoms of toxic shock syndrome.
 XX
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 XX
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 XX
 PN WO9845325-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 01-APR-1998; 98WO-US06663.

XX
 PR 07-APR-1997; 97US-0838413.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 XX
 PI Bannan JD, Zabriskie JB;
 DR WPI: 1998-568335/48.
 XX
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 XX
 PS Claim 4; Page 53; 69pp; English.
 XX
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
 CC Where consensus sequence #1 and #2 are: X25X26YGX1TX2X3X4X5N #1,
 CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
 CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 XX
 SQ Sequence 14 AA:
 Query Match 100.0%; Score 72; DB 19; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CMYGVTEHEGN 12
 Db | | | | | | | | | | | |
 1 cmgygtehegn 12
 RESULT 5
 AAY97840
 ID AAY97840 standard; peptide: 14 AA.
 XX
 AC AAY97840;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6344.
 XX
 KW Pyrogenic exotoxin; enterotoxin; streptococcal infection;
 KW staphylococcal infection; septic shock; toxic shock; vaccine;
 KW antibody.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS Streptococcus sp. 'Group A'.
 XX
 PN WO200020598-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US22180.
 XX
 PR 07-OCT-1998; 98US-0168303.
 PR 18-JUN-1999; 99US-0335581.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.

PI Bannan JD, Visvanathan K, Zabriskie JB;
XX
XX WPI: 2000-303782/26.

PT Peptides useful for preventing and reducing the symptoms of toxic shock
PT syndrome and septic shock from staphylococcal and streptococcal
PT infections -

PS Claim 4: Page 88; 115pp; English.

CC The invention relates to novel peptides (AA97838-197843) comprising a
CC consensus amino acid sequence derived from two conserved regions
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N
CC (AA97863) and consensus region 2a (a preferred consensus region 2) has
CC the sequence K-X6-X7-X8-
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
CC (AA97864), where: X1, X8, X13 and X24 are each independently selected
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
CC the group consisting of any amino acid;
CC X3, X5 and X26 are each independently selected from the group consisting
CC of any amino acid and of no amino acid;
CC X27 is either L or V.

CC The invention also relates to serum antibodies induced by the peptides
CC which provide protection against, or reduce the severity of toxic shock
CC and septic shock caused by the staphylococcal and streptococcal
CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic
CC exotoxins) constitute a family of structurally related toxins which
CC share similar biological activities. They stimulate CD4⁺, CD8⁺ and
CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
CC elements on the lateral face of the T-cell receptor (TCR) while
CC simultaneously binding the lateral face of the class II major
CC histocompatibility complex (MHC) of antigen presenting cells. This causes
CC aberrant proliferation of T-cells, which stimulates other components of
CC the immune system, causing injury to the host. The peptides are used to
CC prevent, treat or protect against toxic shock and septic shock resulting
CC from bacterial infections in mammals, particularly humans. The peptides
CC are used for inducing serum antibodies that bind at least one
CC staphylococcal enterotoxin or streptococcal exotoxin and both the
CC peptides and antibodies can be used in diagnostic assays to aid in the
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
CC acids encoding a peptide of the invention can be used for the production
CC of the peptides for diagnostic reagents, as vaccines and for therapies
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
CC of the peptides can be used in immunotherapy and immunoprophylaxis when
CC expressed in humans. The antibodies are used for passive immunisation
CC therapy to prevent or increase resistance to toxic shock syndrome or
CC septic shock and to ameliorate the effects of conditions associated with
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The
CC amino acid sequences of the peptides are sufficiently common that they
CC can be used for eliciting antibodies which are cross-reactive with toxins
CC derived from various bacteria. Sequences AA97838-197834 represent the
CC synthetic peptides based on consensus consensus regions 1 and 2 of
CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.
CC These peptides can be administered to a mammal to raise serum antibodies
CC for protection against or amelioration of toxic or septic shock.

XX Sequence 14 AA;

Query Match 100.0%; Score 72; DB 21; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTFHEGN 12
XXXXXXXXXXXX
Db 1 cmgygvtehegn 12

RESULT 6

AAV72178
ID AAV72178 standard; peptide: 14 AA.

AC AAV72178;

DT 24-APR-2001 (first entry)

DE Peptide #6344, derived from streptococcal and staphylococcal toxins.

KW Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;

KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;

OS streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.

OS Streptococcus sp.

PM WO200078790-A2.

PD 28-DEC-2000.

PF 16-JUN-2000; 2000WO-US16680.

PR 18-JUN-1999; 99US-0336627.

PA (UVRQ) UNIV ROCKEFELLER.

PI Visvanathan K, Zabriskie JB;

DR WPI: 2001-080820/09.

PT Providing protection against, and reducing the severity of, human
PT immunodeficiency virus infections and associated deleterious effects,
PT using peptides from homologous sequences of staphylococcal and
PT streptococcal toxins -

PS Claim 5; Page 38; 76pp; English.

CC The present sequence is peptide #6344, a cross-linked polymer derived
CC from the homologous sequences of staphylococcal enterotoxin and
CC streptococcal pyrogenic exotoxin.

CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
CC against the peptide are useful for inhibiting blastogenesis of
CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency
CC virus (HIV), inhibiting HIV replication and protecting a mammal against
CC the deleterious effects of HIV. The peptide is also used to ameliorate
CC the effects of autoimmune diseases associated with the presence of HIV.
CC The Ab is used for passively immunising a mammal against the deleterious
CC effects of HIV.

XX Sequence 14 AA;

Query Match 100.0%; Score 72; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTFHEGN 12
XXXXXXXXXXXX
Db 1 cmgygvtehegn 12

RESULT 7

AAW72426
ID AAW72426 standard; peptide: 36 AA.

AC AAW72426;

DT 22-DEC-1998 (first entry)

DE Peptide #5 for reducing symptoms of toxic shock syndrome.

KW Toxic shock syndrome; immunogenic response; bacterial infection;

KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;

KW autoImmune disease.
 XX
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 XX
 PN MO9845325-A1.
 PD 15-OCT-1998.
 XX
 PF 01-APR-1998; 98WO-US06663.
 XX
 PR 07-APR-1997; 97US-0838413.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 PI Bannan JD, Zabriskie JB;
 XX
 DR WPI: 1998-568335/48.
 XX
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoImmune diseases
 PS
 XX Claim 4; Page 54; 69pp; English.
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
 CC Where consensus sequence #1 and #2 are: X25X26YGX17X23X34X5N #1,
 CC K6X78X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
 CC are used: (1) for diagnostic detection of SPEA or SEA, SEB and SED. In
 CC usual immunoassays; (11) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoImmune disease associated with bacterial infections);
 CC and (111) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 XX
 SO Sequence 36 AA:
 Query Match 100.0%; Score 72; DB 19; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CMYGVTFHEGN 12
 DB 1 |||||||||||
 1 cmvgvtehegn 12
 RESULT 8
 AAY97842
 ID AAY97842 standard; peptide: 36 AA.
 XX
 AC AAY97842;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6347.
 XX
 KW Pyrogenic exotoxin; enterotoxin; streptococcal infection;
 KW staphylococcal infection; septic shock; toxic shock; vaccine;
 XX antibody.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS Streptococcus sp. 'Group A'.
 XX

PN WO200020598-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US22180.
 XX
 PR 07-OCT-1998; 98US-0168303.
 PR 18-JUN-1999; 99US-0335581.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 PI Bannan JD, Viswanathan K, Zabriskie JB;
 XX
 DR WPI: 2000-303782/26.
 XX
 PT Peptides useful for preventing and reducing the symptoms of toxic shock
 PT syndrome and septic shock from staphylococcal and streptococcal
 PT infections -
 PS
 XX Claim 4; Page 86; 115pp; English.
 CC The invention relates to novel peptides (AAY97838-Y97843) comprising a
 CC consensus amino acid sequence derived from two conserved regions
 CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
 CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
 CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N
 CC (AAY97863) and consensus region 2a (a preferred consensus region 2) has
 CC the sequence K-X6-X7-X8
 CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
 CC (AAY97864), where: X1, X8, X13 and X24 are each independently selected
 CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
 CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
 CC the group consisting of any amino acid;
 CC X3, X5 and X26 are each independently selected from the group consisting
 CC of any amino acid and of no amino acid;
 CC X27 is either L or Y.
 CC The invention also relates to serum antibodies induced by the peptides
 CC which provide protection against, or reduce the severity of toxic shock
 CC and septic shock caused by the staphylococcal and streptococcal
 CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
 CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic
 CC exotoxins) constitute a family of structurally related toxins which
 CC share similar biological activities. They stimulate CD4+, CD8+ and
 CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
 CC elements on the lateral face of the T-cell receptor (TCR) while
 CC simultaneously binding the lateral face of the class II major
 CC histocompatibility complex (MHC) of antigen presenting cells. This causes
 CC aberrant proliferation of T-cells, which stimulates other components of
 CC the immune system, causing injury to the host. The peptides are used to
 CC prevent, treat or protect against toxic shock and septic shock resulting
 CC from bacterial infections in mammals, particularly humans. The peptides
 CC are used for inducing serum antibodies that bind at least one
 CC staphylococcal enterotoxin or streptococcal exotoxin and both the
 CC peptides and antibodies can be used in diagnostic assays to aid in the
 CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
 CC acids encoding a peptide of the invention can be used for the production
 CC of the peptides for diagnostic reagents, as vaccines and for therapies
 CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
 CC of the peptides can be used in immunotherapy and immunoprophylaxis when
 CC expressed in humans. The antibodies are used for passive immunisation
 CC therapy to prevent or increase resistance to toxic shock syndrome or
 CC septic shock and to ameliorate the effects of conditions associated with
 CC the presence of staphylococcal or streptococcal pyrogenic toxins. The
 CC amino acid sequences of the peptides are sufficiently common that they
 CC can be used for eliciting antibodies which are cross-reactive with toxins
 CC derived from various bacteria. Sequences AAY97838-Y97843 represent the
 CC synthetic peptides based on consensus consensus regions 1 and 2 of
 CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.
 CC These peptides can be administered to a mammal to raise serum antibodies
 CC for protection against or amelioration of toxic or septic shock.
 XX
 SO Sequence 36 AA:

Query Match 100.0%; Score 72; DB 21; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
 |||||
 DB 1 cmgygvtehegn 12

RESULT 9

AAV72180 ID AAV72180 standard; peptide; 36 AA.

XX AC AAV72180;

DT 24-APR-2001 (first entry)

DE Peptide #6347, derived from streptococcal and staphylococcal toxins.

XX Mononuclear cell; blastogenesis; inhibitor: HIV; replication; therapy;

KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;

XX streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.

OS Streptococcus sp.

OS Staphylococcus sp.

PN W0200078790-A2.

PD 28-DEC-2000.

PF 16-JUN-2000; 2000W0-US16680.

PR 18-JUN-1999; 99US-0336627.

PA (UYRQ) UNIV ROCKEFELLER.

PI Visvanathan K, Zabriske JB;

DR WPI; 2001-080820/09.

XX Providing protection against, and reducing the severity of, human

PT immunodeficiency virus infections and associated deleterious effects,

XX using peptides from homologous sequences of staphylococcal and

PT streptococcal toxins

XX Claim 5; Page 38; 76pp; English.

XX The present sequence is peptide #6347, derived from the homologous

CC sequences of staphylococcal enterotoxin and streptococcal pyrogenic

CC exotoxin.

CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced

CC against the peptide are useful for inhibiting blastogenesis of

CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency

CC virus (HIV), inhibiting HIV replication and protecting a mammal against

CC the deleterious effects of HIV. The peptide is also used to ameliorate

CC the effects of autoimmune diseases associated with the presence of HIV.

CC The Ab is used for passively immunising a mammal against the deleterious

CC effects of HIV.

SQ Sequence 36 AA;

Query Match 100.0%; Score 72; DB 22; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
 |||||
 DB 1 cmgygvtehegn 12

RESULT 10

AAW72427 ID AAW72427 standard; peptide; 38 AA.

XX AC AAW72427;

DT 22-DEC-1998 (first entry)

DE Peptide #6 for reducing symptoms of toxic shock syndrome.

XX Toxic shock syndrome; immunogenic response; bacterial infection;

KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;

XX autoimmune disease.

OS Synthetic.

OS Staphylococcus sp.

OS Streptococcus sp.

PN W09845325-A1.

PD 15-OCT-1998.

PF 01-APR-1998; 98W0-US06663.

PR 07-APR-1997; 97US-0838413.

PA (UYRQ) UNIV ROCKEFELLER.

PI Bannan JD, Zabriske JB;

DR WPI; 1998-568335/48.

XX New peptides that generate antibodies against staphylococcal and

PT streptococcal toxins - used to diagnose, treat or prevent toxic

PT shock and autoimmune diseases

XX Claim 4; Page 54; 69pp; English.

XX The present invention describes peptides having consensus sequences #1

CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.

CC Where consensus sequence #1 and #2 are: X25X26YGX1X2X3X4X5N #1,

CC KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where

CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)

CC or are absent; X27 = L or Y; all other X may be any aa. The peptides

CC can be used to generate serum antibodies (Ab) that bind at least one

CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab

CC are used: (i) for diagnostic detection of SPEA or SPE, SEB and SED, in

CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear

CC cells in presence of these toxins (i.e. to protect against or alleviate

CC toxic shock or autoimmune disease associated with bacterial infections);

CC and (iii) for passive immunisation against effects of the toxins. The

CC peptides generate Ab that are cross-reactive with toxins from a variety

CC of bacteria. The present sequence represents a specifically claimed

CC example of a peptide of the present invention.

SQ Sequence 38 AA;

Query Match 100.0%; Score 72; DB 19; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
 |||||
 DB 1 cmgygvtehegn 12

RESULT 11

AAV97843 ID AAV97843 standard; peptide; 38 AA.

XX AC AAV97843;

DT 29-AUG-2000 (first entry)

XX Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6348.
 DE
 XX
 XX Pyrogenic exotoxin; enterotoxin; streptococcal infection;
 KW
 KW staphylococcal infection; septic shock; toxic shock; vaccine;
 KM
 KM antibody.
 XX
 XX Synthetic.
 OS
 OS Staphylococcus aureus.
 OS Streptococcus sp. 'Group A'.
 XX
 PN W0200020598-A1.
 PD 13-APR-2000.
 XX
 XX 24-SEP-1999; 99WO-US22180.
 PF
 XX 07-OCT-1998; 98US-0168303.
 PR 18-JUN-1999; 99US-0335581.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 Bannan JD, Viswanathan K, Zabriskie JB;
 P1
 DR WPI: 2000-303782/26.
 XX
 XX
 PT Peptides useful for preventing and reducing the symptoms of toxic shock
 PT syndrome and septic shock from staphylococcal and streptococcal
 PT infections -
 XX
 PS Claim 4; Page 88; 115pp: English.
 XX
 CC The invention relates to novel peptides (AAV97838-Y97843) comprising a
 CC consensus amino acid sequence derived from two conserved regions
 CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
 CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
 CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N
 CC (AAV97863) and consensus region 2a (a preferred consensus region 2) has
 CC the sequence K-X6-X7-X8-
 CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
 CC (AAV97864), where: X1, X8, X13 and X24 are each independently selected
 CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
 CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
 CC the group consisting of any amino acid;
 CC X3, X5 and X26 are each independently selected from the group consisting
 CC of any amino acid and of no amino acid;
 CC X27 is either L or Y.
 CC The invention also relates to serum antibodies induced by the peptides
 CC which provide protection against, or reduce the severity of toxic shock
 CC and septic shock caused by the staphylococcal and streptococcal
 CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
 CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic
 CC exotoxins) constitute a family of structurally related toxins which
 CC share similar biological activities. They stimulate CD4+, CD8+ and
 CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
 CC elements on the lateral face of the T-cell receptor (TCR) while
 CC simultaneously binding the lateral face of the class II major
 CC histocompatibility complex (MHC) of antigen presenting cells. This causes
 CC aberrant proliferation of T-cells, which stimulates other components of
 CC the immune system, causing injury to the host. The peptides are used to
 CC prevent, treat or protect against toxic shock and septic shock resulting
 CC from bacterial infections in mammals, particularly humans. The peptides
 CC are used for inducing serum antibodies that bind at least one
 CC staphylococcal enterotoxin or streptococcal exotoxin and both the
 CC peptides and antibodies can be used in diagnostic assays to aid in the
 CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
 CC acids encoding a peptide of the invention can be used for the production
 CC of the peptides for diagnostic reagents, as vaccines and for therapies
 CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
 CC of the peptides can be used in immunotherapy and immunoprophylaxis when
 CC expressed in humans. The antibodies are used for passive immunisation
 CC therapy to prevent or increase resistance to toxic shock syndrome or
 CC septic shock and to ameliorate the effects of conditions associated with

CC the presence of staphylococcal or streptococcal pyrogenic toxins. The
 CC amino acid sequences of the peptides are sufficiently common that they
 CC can be used for eliciting antibodies which are cross-reactive with toxins
 CC derived from various bacteria. Sequences AAV97838-Y97843 represent the
 CC synthetic peptides based on consensus consensus regions 1 and 2 of
 CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.
 CC These peptides can be administered to a mammal to raise serum antibodies
 CC for protection against or amelioration of toxic or septic shock.
 CC
 XX
 SQ Sequence 38 AA;
 Query Match 100.0%; Score 72; DB 21; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1,2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CMYGVTEHEGN 12
 DB 1 CMYGVTEHEGN 12
 RESULT 12
 AAV72181
 ID AAV72181 standard; peptide; 38 AA.
 XX
 AC AAV72181;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Peptide #6348, derived from streptococcal and staphylococcal toxins.
 XX
 KW Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
 KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;
 KW streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.
 XX
 OS Streptococcus sp.
 OS Staphylococcus sp.
 PN W0200078790-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000WO-US16680.
 XX
 PR 18-JUN-1999; 99US-0336627.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Viswanathan K, Zabriskie JB;
 P1
 DR WPI: 2001-080820/09.
 XX
 PT Providing protection against, and reducing the severity of, human
 PT immunodeficiency virus infections and associated deleterious effects,
 PT using peptides from homologous sequences of staphylococcal and
 PT streptococcal toxins -
 XX
 PS Claim 5; Page 38; 76pp: English.
 XX
 CC The present sequence is peptide #6348, a cross-linked polymer derived
 CC from the homologous sequences of staphylococcal enterotoxin and
 CC streptococcal pyrogenic exotoxin.
 CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
 CC against the peptide are useful for inhibiting blastogenesis of
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against
 CC the deleterious effects of HIV. The peptide is also used to ameliorate
 CC the effects of autoimmune diseases associated with the presence of HIV.
 CC The Ab is used for passively immunising a mammal against the deleterious
 CC effects of HIV.
 XX
 SO Sequence 38 AA;

Query Match 100.0%; Score 72; DB 22; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
 |||||||
 Db 1 cmvgvtehegn 12

RESULT 13
 AAY97845
 ID AAY97845 standard; peptide; 12 AA.
 AC AAY97845;
 XX 29-AUG-2000 (first entry)
 DT 29-AUG-2000 (first entry)
 DE Staphylococcus aureus enterotoxin SEB, conserved region 1.
 XX Staphylococcal infection; enterotoxin; septic shock; toxic shock;
 KW vaccine; antibody.
 XX Staphylococcus aureus.
 OS Staphylococcus aureus.
 XX WO200020598-A1.
 PN 13-APR-2000.
 PD 13-APR-2000.
 XX 24-SEP-1999; 99WO-US22180.
 PF 24-SEP-1999; 99WO-US22180.
 XX 07-OCT-1998; 98US-0168303.
 PR 18-JUN-1999; 99US-0335581.
 XX (UTRQ) UNIV ROCKEFELLER.
 PA Bannan JD, Visvanathan K, Zabriskie JB;
 XX WPI: 2000-303782/26.
 DR WPI: 2000-303782/26.
 XX Peptides useful for preventing and reducing the symptoms of toxic shock
 PT syndrome and septic shock from staphylococcal and streptococcal
 PT infections -
 PS Example 1; Page 72; 115pp; English.

The invention relates to novel peptides (AAY97838-Y97843) comprising a
 CC consensus amino acid sequence derived from two conserved regions
 CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
 CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
 CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N
 CC (AAY97863) and consensus region 2a (a preferred consensus region 2) has
 CC the sequence K-X6-X7-X8-
 CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
 CC (AAY97864), where: X1, X8, X13 and X24 are each independently selected
 CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
 CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
 CC the group consisting of any amino acid;
 CC X3, X5 and X26 are each independently selected from the group consisting
 CC of any amino acid and of no amino acid;
 CC X27 is either L or Y.

The invention also relates to serum antibodies induced by the peptides
 CC which provide protection against, or reduce the severity of toxic shock
 CC and septic shock caused by the staphylococcal and streptococcal
 CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
 CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic
 CC exotoxins) constitute a family of structurally related toxins which
 CC share similar biological activities. They stimulate CD4+, CD8+ and
 CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
 CC elements on the lateral face of the T-cell receptor (TCR) while
 CC simultaneously binding the lateral face of the class II major
 CC histocompatibility complex (MHC) of antigen presenting cells. This causes
 CC aberrant proliferation of T-cells, which stimulates other components of

CC the immune system, causing injury to the host. The peptides are used to
 CC prevent, treat or protect against toxic shock and septic shock resulting
 CC from bacterial infections in mammals, particularly humans. The peptides
 CC are used for inducing serum antibodies that bind at least one
 CC staphylococcal enterotoxin or streptococcal exotoxin and both the
 CC peptides and antibodies can be used in diagnostic assays to aid in the
 CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
 CC acids encoding a peptide of the invention can be used for the production
 CC of the peptides for diagnostic reagents, as vaccines and for therapies
 CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
 CC of the peptides can be used in immunotherapy and immunoprophylaxis when
 CC expressed in humans. The antibodies are used for passive immunisation
 CC therapy to prevent or increase resistance to toxic shock syndrome or
 CC septic shock and to ameliorate the effects of conditions associated with
 CC the presence of staphylococcal or streptococcal pyrogenic toxins. The
 CC amino acid sequences of the peptides are sufficiently common that they
 CC can be used for eliciting antibodies which are cross-reactive with toxins
 CC derived from various bacteria. Sequences AAY97844-Y97852 represent
 CC conserved region 1 of various staphylococcus aureus enterotoxins and
 CC Group A streptococcal pyrogenic exotoxins.

Sequence 12 AA;
 SQ

Query Match 93.1%; Score 67; DB 21; Length 12;
 Best Local Similarity 91.7%; Pred. No. 2.6e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
 |||||||
 Db 1 cmvgvtehegn 12

RESULT 14
 AAY97846
 ID AAY97846 standard; peptide; 12 AA.
 AC AAY97846;
 XX 29-AUG-2000 (first entry)
 DT 29-AUG-2000 (first entry)
 DE Staphylococcus aureus enterotoxin SEC, conserved region 1.
 XX Staphylococcal infection; enterotoxin; septic shock; toxic shock;
 KW vaccine; antibody.
 XX Staphylococcus aureus.
 OS Staphylococcus aureus.
 XX WO200020598-A1.
 PN 13-APR-2000.
 PD 13-APR-2000.
 XX 24-SEP-1999; 99WO-US22180.
 PF 24-SEP-1999; 99WO-US22180.
 XX 07-OCT-1998; 98US-0168303.
 PR 18-JUN-1999; 99US-0335581.
 XX (UTRQ) UNIV ROCKEFELLER.
 PA Bannan JD, Visvanathan K, Zabriskie JB;
 XX WPI: 2000-303782/26.
 DR WPI: 2000-303782/26.
 XX Peptides useful for preventing and reducing the symptoms of toxic shock
 PT syndrome and septic shock from staphylococcal and streptococcal
 PT infections -
 PS Example 1; Page 72; 115pp; English.

The invention relates to novel peptides (AAY97838-Y97843) comprising a
 CC consensus amino acid sequence derived from two conserved regions
 CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
 CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred

consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N (AA97863) and consensus region 2a (a preferred consensus region 2) has the sequence K-X6-X7-X8-X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y (AA97864), where: X1, X8, X13 and X24 are each independently selected from L, I and V, X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16, X17, X18, X19, X20, X21, X22 and X23 are each independently selected from the group consisting of any amino acid; X3, X5 and X26 are each independently selected from the group consisting of any amino acid and of no amino acid; X27 is either L or Y.

The invention also relates to serum antibodies induced by the peptides which provide protection against, or reduce the severity of toxic shock and septic shock caused by the staphylococcal and streptococcal pyrogenic toxins. The pyrogenic exotoxins of Group A streptococcal and the enterotoxins of *Staphylococcus aureus* (which are also pyrogenic exotoxins) constitute a family of structurally related toxins which share similar biological activities. They stimulate CD4⁺, CD8⁺ and gamma-delta⁺ T-cells by binding the beta-chain variable region (V-beta) elements on the lateral face of the T-cell receptor (TCR) while simultaneously binding the lateral face of the class II major histocompatibility complex (MHC) of antigen presenting cells. This causes aberrant proliferation of T-cells, which stimulates other components of the immune system, causing injury to the host. The peptides are used to prevent, treat or protect against toxic shock and septic shock resulting from bacterial infections in mammals, particularly humans. The peptides are used for inducing serum antibodies that bind at least one staphylococcal enterotoxin or streptococcal exotoxin and both the peptides and antibodies can be used in diagnostic assays to aid in the diagnosis of disease related to the presence of bacterial toxins. Nucleic acids encoding a peptide of the invention can be used for the production of the peptides for diagnostic reagents, as vaccines and for therapies for pyrogenic exotoxin related diseases. Vectors expressing high levels of the peptides can be used in immunotherapy and immunoprophylaxis when expressed in humans. The antibodies are used for passive immunisation therapy to prevent or increase resistance to toxic shock syndrome or septic shock and to ameliorate the effects of conditions associated with the presence of staphylococcal or streptococcal pyrogenic toxins. The amino acid sequences of the peptides are sufficiently common that they can be used for eliciting antibodies which are cross-reactive with toxins derived from various bacteria. Sequences AA97844-Y97852 represent conserved region 1 of various *Staphylococcus aureus* enterotoxins and Group A streptococcal pyrogenic exotoxins.

Sequence 12 AA:

Query Match 93.1%; Score 67; DB 21; Length 12;
Best Local Similarity 83.3%; Pred. NO. 2.6e-05;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 1 CMYGVTREHGN 12
|||||:|||||
Db 1 cmvgjltkhegn 12

RESULT 15
AA972183
AA972183 standard; peptide: 12 AA.

XX AAY72183:
XX
XX
DT 24-APR-2001 (first entry)
XX
XX Peptide from region 1 of staphylococcal enterotoxin SEB.
XX
XX Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
KM staphylococcal enterotoxin; human immunodeficiency virus; T cell;
KM autoimmune disease; immunisation.
XX
OS Staphylococcus sp.
XX
NN MO200078790-A2.

XX 28-DEC-2000.
PD
XX
XX 16-JUN-2000; 2000MO-US16680.
PF
XX 18-JUN-1999; 9905-0336627.
PR
XX
XX (UVRQ) UNIV ROCKEFELLER.
PA
XX
PI Visvanathan K, Zabriskie JB;
XX
XX WPI: 2001-080820/09.
DR
XX
XX Providing protection against, and reducing the severity of, human
PT immunodeficiency virus infections and associated deleterious effects,
PT using peptides from homologous sequences of staphylococcal and
PT streptococcal toxins -
XX
XX
PS Disclosure; Page 36; 76pp; English.
XX
XX
XX The present sequence is a peptide from region 1 of staphylococcal
CC enterotoxin SEB.
CC
CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
CC against the peptide are useful for inhibiting blastogenesis of
CC monoclonal cells (eg. T cells) in the presence of human immunodeficiency
CC virus (HIV), inhibiting HIV replication and protecting a mammal against
CC the deleterious effects of HIV. The peptide is also used to ameliorate
CC the effects of autoimmune diseases associated with the presence of HIV.
CC The Ab is used for passively immunising a mammal against the deleterious
CC effects of HIV.
XX
XX
SQ Sequence 12 AA;
XX

```

Query Match          93.1%  Score 67:  DB 22:  Length 12:
Best Local Similarity 91.7%  Pred. No. 2.6e-05;
Matches    11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0
Oy         1  CMYGGVTEHEGN 12
           | | | | | | | | | |
Db         1  CMYGGVTEHNGN 12

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Job time: 10129 sec

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Search completed: January 2, 2002, 20:48:13

Job time: 10129 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 17:35:14 ; Search time 40.75 Seconds
(without alignments)
6.627 Million cell updates/sec

Title: US-09-335-581A-3

Perfect score: 72
Sequence: 1 CMYGVTEHGN 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	72	100.0	12	3	US-08-838-413A-3	Sequence 3, Appl1
2	72	100.0	14	3	US-08-838-413A-5	Sequence 5, Appl1
3	72	100.0	36	3	US-08-838-413A-7	Sequence 7, Appl1
4	72	100.0	38	3	US-08-838-413A-8	Sequence 8, Appl1
5	67	93.1	12	3	US-08-838-413A-10	Sequence 10, Appl1
6	67	93.1	12	3	US-08-838-413A-11	Sequence 11, Appl1
7	67	93.1	13	4	US-08-896-933-3	Sequence 3, Appl1
8	67	93.1	14	4	US-08-896-933-5	Sequence 5, Appl1
9	67	93.1	238	4	US-08-896-933-28	Sequence 28, Appl1
10	67	93.1	239	4	US-08-896-933-26	Sequence 26, Appl1
11	67	93.1	239	4	US-08-896-933-27	Sequence 27, Appl1
12	67	93.1	255	1	US-08-446-918A-2	Sequence 2, Appl1
13	67	93.1	255	1	US-08-580-806-2	Sequence 2, Appl1
14	64	88.9	14	4	US-08-896-933-13	Sequence 13, Appl1
15	64	88.9	220	4	US-08-896-933-20	Sequence 20, Appl1
16	63	87.5	12	3	US-08-838-413A-15	Sequence 15, Appl1
17	63	87.5	14	4	US-08-896-933-11	Sequence 11, Appl1
18	63	87.5	221	4	US-08-896-933-29	Sequence 29, Appl1
19	60	83.3	12	3	US-08-838-413A-12	Sequence 12, Appl1
20	60	83.3	14	4	US-08-896-933-7	Sequence 7, Appl1
21	59	83.3	228	4	US-08-896-933-25	Sequence 25, Appl1
22	59	81.9	12	3	US-08-838-413A-17	Sequence 17, Appl1
23	59	81.9	239	4	US-08-896-933-21	Sequence 21, Appl1
24	55	76.4	12	3	US-08-838-413A-9	Sequence 9, Appl1
25	55	76.4	12	3	US-08-838-413A-13	Sequence 13, Appl1
26	55	76.4	12	3	US-08-838-413A-30	Sequence 30, Appl1
27	55	76.4	14	4	US-08-896-933-1	Sequence 1, Appl1

28	55	76.4	14	4	US-08-896-933-9	Sequence 9, Appl1
29	55	76.4	23	1	US-08-220-378-5	Sequence 5, Appl1
30	55	76.4	23	2	US-08-696-012-5	Sequence 24, Appl1
31	55	76.4	226	4	US-08-896-933-24	Sequence 23, Appl1
32	55	76.4	232	4	US-08-896-933-23	Sequence 4, Appl1
33	55	76.4	233	2	US-08-446-918A-4	Sequence 4, Appl1
34	55	76.4	233	2	US-08-580-806-4	Sequence 112, App
35	55	76.4	257	3	US-08-486-099-112	Sequence 122, App
36	55	76.4	257	3	US-08-486-099-113	Sequence 123, App
37	55	76.4	257	3	US-08-360-107A-122	Sequence 112, App
38	55	76.4	257	3	US-08-360-107A-123	Sequence 113, App
39	55	76.4	257	3	US-08-484-223B-112	Sequence 112, App
40	55	76.4	257	3	US-08-484-223B-113	Sequence 113, App
41	55	76.4	257	3	US-08-919-597-112	Sequence 113, App
42	55	76.4	257	3	US-08-919-597-113	Sequence 112, App
43	55	76.4	257	3	US-08-475-668A-112	Sequence 113, App
44	55	76.4	257	3	US-08-475-668A-113	Sequence 112, App
45	55	76.4	257	3	US-08-485-551A-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-08-838-413A-3
; Sequence 3, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES USEFUL FOR
; TITLE OR INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,413A
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2016-4010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
; US-08-838-413A-3
Query Match 100.0%; Score 72; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHEGN 12
|||||
Db 1 CMYGVTEHEGN 12

RESULT 2
US-08-838-413A-5
; Sequence 5, Application us/08838413A
; Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)751-6849

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 14

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-5

Query Match

Best Local Similarity 100.0%; Score 72; DB 3; Length 14;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHEGN 12

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Db 1 CMYGVTEHEGN 12

RESULT 3

US-08-838-413A-7

; Sequence 7, Application us/08838413A

; Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2016-4010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)751-6849

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: AMINO ACID

STRANDEDNESS: UNKNOWN

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PEPTIDE

US-08-838-413A-7

Query Match

Best Local Similarity 100.0%; Score 72; DB 3; Length 36;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHEGN 12

|||||

Db 1 CMYGVTEHEGN 12

RESULT 4

US-08-838-413A-8

; Sequence 8, Application us/08838413A

; Patent No. 6075119

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PEPTIDES USEFUL FOR

TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,413A

FILING DATE: 07-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

;; FILING DATE:
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MORRY, MARY J.
;; REGISTRATION NUMBER: 34,398
;; REFERENCE/DOCKET NUMBER: 2016-4010
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)751-6800
;; TELEFAX: (212)751-6849
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38
;; TYPE: AMINO ACID
;; STRANDEDNESS: UNKNOWN
;; TOPOLOGY: UNKNOWN
;; MOLECULE TYPE: PEPTIDE
;; US-08-838-413A-8

Query Match 100.0%; Score 72; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CMYGVTEHGN 12
Db 1 CMYGVTEHGN 12

RESULT 5
US-08-838-413A-10
; Sequence 10, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES USEFUL FOR
; TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,413A
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2016-4010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)751-6800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
; US-08-838-413A-10

Query Match 93.1%; Score 67; DB 3; Length 12;
Best Local Similarity 91.7%; Pred. No. 2.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CMYGVTEHGN 12
Db 1 CMYGVTEHGN 12

RESULT 6
US-08-838-413A-11
; Sequence 11, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES USEFUL FOR
; TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,413A
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2016-4010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)751-6800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
; US-08-838-413A-11

Query Match 93.1%; Score 67; DB 3; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.8e-05;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CMYGVTEHGN 12
Db 1 CMYGVTEHGN 12

RESULT 7
US-08-896-933-3
; Sequence 3, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

```
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER APPLICATION NUMBER: 08/252,978  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-3
```

```
Query Match          93.1%; Score 67; DB 4; Length 13;  
Best Local Similarity 91.7%; Pred. No. 3e-05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 CMYGVTEHGN 12  
        |||||:||||  
Db      1 CMYGVTEHGN 12
```

```
RESULT      8  
US-08-896-933-5  
; Sequence 5, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER APPLICATION NUMBER: 08/252,978  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-5
```

```
Query Match          93.1%; Score 67; DB 4; Length 14;  
Best Local Similarity 83.3%; Pred. No. 3.2e-05;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CMYGVTEHGN 12  
        |||||:||||  
Db      1 CMYGVTEHGN 12
```

```
RESULT      9  
US-08-896-933-28  
; Sequence 28, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER APPLICATION NUMBER: 08/252,978  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 238
```

```
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-28
```

```
Query Match          93.1%; Score 67; DB 4; Length 238;  
Best Local Similarity 83.3%; Pred. No. 0.00061;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CMYGVTEHGN 12  
        |||||:||||  
Db      109 CMYGVTEHGN 120
```

```
RESULT      10  
US-08-896-933-26  
; Sequence 26, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER APPLICATION NUMBER: 08/252,978  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-26
```

```
Query Match          93.1%; Score 67; DB 4; Length 239;  
Best Local Similarity 91.7%; Pred. No. 0.00061;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 CMYGVTEHGN 12  
        |||||:||||  
Db      113 CMYGVTEHGN 124
```

```
RESULT      11  
US-08-896-933-27  
; Sequence 27, Application US/08896933  
; Patent No. 6221351  
; GENERAL INFORMATION:  
; APPLICANT: Terman, David S.  
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,  
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS  
; FILE REFERENCE: 09629/005002  
; CURRENT APPLICATION NUMBER: US/08/896,933  
; CURRENT FILING DATE: 1997-07-18  
; EARLIER APPLICATION NUMBER: 08/252,978  
; EARLIER FILING DATE: 1994-06-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureas  
US-08-896-933-27
```

```
Query Match          93.1%; Score 67; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 0.00061;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CMYGVTEHGN 12  
        |||||:||||
```

DB 110 CMYGGTTEHGN 121

RESULT 12

US-08-446-918A-2

Sequence 2, Application US/08446918A

Patent No. 5705151

GENERAL INFORMATION:

APPLICANT: Dow, Steve W.

APPLICANT: Elmslie, Robyn E.

TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: U.S.A.

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,918A

FILING DATE: 18-MAY-1995

CLASSIFICATION: 552

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.

REGISTRATION NUMBER: 33,005

REFERENCE/DOCKET NUMBER: 2879-29

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 255 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-446-918A-2

Query Match 93.1%; Score 67; DB 1; Length 255;

Best Local Similarity 91.7%; Pred. No. 0.00065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGTTEHGN 12

DB 129 CMYGGTTEHGN 140

RESULT 13

US-08-580-806-2

Sequence 2, Application US/08580806

Patent No. 5935568

GENERAL INFORMATION:

APPLICANT: Dow, Steve W.

APPLICANT: Elmslie, Robyn E.

APPLICANT: Potter, Terence A.

TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver

STATE: Colorado

COUNTRY: U.S.A.

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/580,806

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2879-29-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 255 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-580-806-2

Query Match 93.1%; Score 67; DB 2; Length 255;

Best Local Similarity 91.7%; Pred. No. 0.00065;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGTTEHGN 12

DB 129 CMYGGTTEHGN 140

RESULT 14

US-08-896-933-13

Sequence 13, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

FILE REFERENCE: 09629/005002

CURRENT APPLICATION NUMBER: US/08/896,933

CURRENT FILING DATE: 1997-07-18

EARLIER APPLICATION NUMBER: 08/252,978

EARLIER FILING DATE: 1994-06-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 14

TYPE: PRT

ORGANISM: Other

FEATURE:

OTHER INFORMATION: Consensus sequences derived from staphylococcus

OTHER INFORMATION: aureus and streptococcus pyogenes polypeptides

US-08-896-933-13

Query Match 88.9%; Score 64; DB 4; Length 14;

Best Local Similarity 91.7%; Pred. No. 0.0001;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGTTEHGN 12

DB 1 CMYGGTTEHGN 12

RESULT 15

US-08-896-933-20

Sequence 20, Application US/08896933

Patent No. 6221351

GENERAL INFORMATION:

APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

```

; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 20
; LENGTH: 220
; TYPE: PR1
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20

```

```

Query Match      88.9%; Score 64; DB 4; Length 220;
Best Local Similarity 83.3%; Pred. No. 0.0018;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGYTEHEGN 12
   1:||||| |||
Db 98 CLYGYVTNHEGN 109

```

Search completed: January 2, 2002, 20:46:42
 Job time: 11488 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2002, 20:36:20 ; Search time 56.72 Seconds

(without alignments)
16.116 Million cell updates/sec

Title: US-09-335-581A-3
Perfect score: 72
Sequence: 1 CMGCGVTEHGN 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	93.1	266	1 ENSAB6	enterotoxin B prec
2	67	93.1	266	1 ENSAC1	enterotoxin C-1 pr
3	67	93.1	266	2 A60114	enterotoxin C-2 pr
4	67	93.1	266	2 S11885	enterotoxin C3 - S
5	64	88.9	250	1 A26152	streptococcal pyro
6	63	87.5	236	2 S18789	exotoxin A precus
7	63	87.5	236	2 S18786	exotoxin type A pr
8	63	87.5	236	2 S18783	exotoxin type A pr
9	63	87.5	251	1 S29659	exotoxin type A pr
10	60	83.3	258	2 A33953	enterotoxin D prec
11	55	76.4	257	2 A28664	enterotoxin A prec
12	55	76.4	257	2 A28179	enterotoxin E prec
13	46	63.9	270	2 B48826	high chorioleptic h
14	46	63.9	279	2 C48826	high chorioleptic h
15	45	62.5	366	2 T25259	hypothetical prote
16	45	62.5	375	2 T27314	hypothetical prote
17	42	58.3	203	2 T06277	MADS box protein A
18	41	56.9	151	2 S43727	hypothetical prote
19	41	56.9	644	2 D71427	receptor-like prot
20	41	56.9	664	2 T51247	ARR1 protein [limp
21	41	56.9	669	2 T51246	ARR1 protein [limp
22	40	55.6	185	2 S04792	mobilization prote
23	40	55.6	303	2 C34504	heterogeneous ribo
24	40	55.6	347	2 T35013	probable membrane
25	40	55.6	380	2 G01639	transmembrane prot
26	40	55.6	388	2 T09085	hypothetical prote
27	40	55.6	413	2 E65088	hypothetical prote
28	40	55.6	455	2 T15581	hypothetical prote
29	40	55.6	747	2 B83029	conserved hypotet

30	40	55.6	789	2 A62166	conserved hypotet
31	40	55.6	813	2 T40622	translation elonga
32	40	55.6	877	2 S65057	alpha-glucosidase
33	39	54.2	324	2 T26790	hypothetical prote
34	39	54.2	384	2 T19427	hypothetical prote
35	39	54.2	384	2 T19423	hypothetical prote
36	39	54.2	422	2 F75151	hypothetical prote
37	39	54.2	424	2 D71192	hypothetical prote
38	39	54.2	1827	2 T34288	hypothetical prote
39	38	52.8	198	2 S54733	ribosomal protein
40	38	52.8	242	2 S30238	finger protein ZNF
41	38	52.8	437	2 S69881	phosphopyruvate hy
42	38	52.8	437	2 S67305	phosphopyruvate hy
43	38	52.8	444	2 T15310	hypothetical prote
44	38	52.8	472	2 T45219	regulator of prem
45	38	52.8	628	2 T09458	numb-binding prote

ALIGNMENTS

RESULT 1
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MUID:86168029
A:Accession: S27360
A:Molecule type: DNA
A:Residues: 1-266 <JON>
A:Cross-references: EMBL:M1118; NID:g152939; PIDN:AA88550.1; PID:g153000
R:Experimental source: strain S6
J. Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bro
A:Reference number: A92065; MUID:71007902
A:Accession: A92065
A:Molecule type: Protein
A:Residues: 28-55, 'ND', '59-68, 'NE', '71, 'FDLRYL', '76-117, '119-127, 'N', '129, 'D', '131-132, 'EN
R:Experimental source: strain S-6
J. Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compos
A:Reference number: A92064; MUID:71007901
A:Contents: annotation: chymotryptic peptides
J. Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compos
A:Reference number: A92063; MUID:71007900
A:Contents: annotation: tryptic peptides
R.Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A:Title: Purification of staphylococcal enterotoxin B.
A:Reference number: A90548; MUID:66035792
A:Contents: annotation: biological source of protein
R.Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sves
Eur. J. Biochem. 209, 823-828, 1992
A:Title: Identification of functionally active fragments of staphylococcal enterotoxi
A:Reference number: S27240; MUID:93049338
A:Accession: S27240
A:Molecule type: Protein
A:Residues: 28-42, '128-148 <ALA>
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin; extracellular protein; toxin
F:1-27/Domain: signal sequence #status predicted <Sig>
F:28-266/Product: enterotoxin B #status experimental <MAY>
F:120-140/Disulfide bonds: #status experimental

Query Match 93.1%; Score 67; DB 1; Length 266;
Best Local Similarity 91.7%; Pred. No. 0.00017;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12
DB 140 CMYGVTEHNGN 151

RESULT 2

ENSAC1

enterotoxin C-1 precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
C:Accession: S06356; A01816
R:Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness
A:Reference number: S06356; MUID:88038352
A:Accession: S06356
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Cross-references: EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
R:Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A:Reference number: A01816; MUID:83213327
A:Accession: A01816
A:Molecule type: protein
A:Residues: 28-75, 'IL', '78-176, 'N', '178-266 <SCH>
C:Genetics:
A:Gene: entC1
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-1 #status experimental <MAT>
F:120-137/Disulfide bonds: #status experimental

Query Match 93.1%; Score 67; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 0.00017;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12
DB 137 CMYGVTEHNGN 148

RESULT 3

A60114

enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A:Reference number: A60114; MUID:89277549
A:Accession: A60114
A:Molecule type: DNA
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Accession: B60114
A:Molecule type: protein
A:Residues: 28-66 <BOH2>
R:Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
A:Reference number: A33866; MUID:89327174
A:Accession: A33866
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-266 <COU>
A:Cross-references: GB:M28364; NID:9153003; PIDN:AAA26624.1; PID:9153004
C:Genetics:
A:Gene: entC2
C:Superfamily: enterotoxin B
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 93.1%; Score 67; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 0.00017;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12
DB 137 CMYGVTEHNGN 148

RESULT 4

S11885

enterotoxin C3 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C:Accession: S11885
R:Howde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comp
A:Reference number: S11885; MUID:90220508
A:Accession: S11885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <HOV>
A:Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C:Superfamily: enterotoxin B

Query Match 93.1%; Score 67; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 0.00017;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12
DB 137 CMYGVTEHNGN 148

RESULT 5

A26152

streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (spear)
C:Species: Streptococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26152
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to
A:Reference number: A26152; MUID:86284313
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 88.9%; Score 64; DB 1; Length 250;
Best Local Similarity 83.3%; Pred. No. 0.00054;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12
DB 128 CLYGVTEHNGN 139

RESULT 6

S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18789
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18789
R:Neelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61573; NID:q47303; PIDN:CAA43771.1; PID:q47304
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>
Query Match 87.5% Score 63; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 0.00078;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CMYCGTTEHGN 12
1:||||| ||||
Db 120 CTVGVTNHEGN 131
RESULT 7
S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isol
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain
Isolate United Kingdom; strain MGAS496 isolate Germany
C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R:Neelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323
A:Accession: S18786
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61561; NID:q47297; PIDN:CAA43759.1; PID:q47298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18787
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61562; NID:q47299; PIDN:CAA43760.1; PID:q47300
A:Experimental source: strain MGAS251 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61563; NID:q47301; PIDN:CAA43761.1; PID:q47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61564; NID:q47305; PIDN:CAA43762.1; PID:q47306

A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18792
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61565; NID:q47311; PIDN:CAA43763.1; PID:q47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18795
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61566; NID:q47317; PIDN:CAA43764.1; PID:q47318
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18799
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61567; NID:q47325; PIDN:CAA43765.1; PID:q47326
A:Experimental source: strain MGAS496 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
Query Match 87.5% Score 63; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 0.00078;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CMYCGTTEHGN 12
1:||||| ||||
Db 120 CTVGVTNHEGN 131
RESULT 8
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 1
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain
C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18783; S18793; S18794; S18801; S18798
R:Neelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene en
A:Reference number: S18782; MUID:92044323
A:Accession: S18783
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61568; NID:q47289; PIDN:CAA43766.1; PID:q47290
A:Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18793
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61569; NID:q47313; PIDN:CAA43767.1; PID:q47314
A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61570; NID:q47315; PIDN:CAA43768.1; PID:q47316
A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18801
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334
A:Experimental source: Streptococcus pyogenes strain MGAS624 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18798
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A:Experimental source: Streptococcus pyogenes strain MGAS495 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA3
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 87.5%; Score 63; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 0.00078;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12
I:|||||
Db 120 CTYGVTHNGN 131

RESULT 9
S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N:Alternate names: erythrogenic toxin; scarlet fever toxin
C:Species: Streptococcus pyogenes phage T12
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R:Weeks, C.R.; Ferretti, J.J.
I:Infect. Immun. 52, 144-150, 1986
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g
A:Reference number: S29659; MUID:86166804
A:Accession: S29659
A:Molecule type: DNA
A:Residues: 1-251 <NE>
A:Cross-references: GB:U04053; EMBL:M19350; NID:g1877426; PIDN:AAC48868.1; PID:g1877430
J:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
R:Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323
A:Accession: S18782
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288
A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18784
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18785
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294
A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned ph
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18791
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18796
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320
A:Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18797
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18800
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-228 <NE>
A:Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328
A:Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 87.5%; Score 63; DB 1; Length 251;
Best Local Similarity 83.3%; Pred. No. 0.00083;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 CMYGVTEHNGN 12
I:|||||
Db 128 CTYGVTHNGN 139

RESULT 10
A33953
enterotoxin D precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C:Accession: A33953
R:Bayles, R.W.; Iandolo, J.J.
J:Bacteriol. 171, 4799-4806, 1989
A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotox
A:Reference number: A33953; MUID:89355112
A:Accession: A33953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <BAV>
A:Cross-references: GB:M28521; NID:g1492109; PIDN:AA06195.1; PID:g758691
C:Superfamily: enterotoxin B

Query Match 83.3%; Score 60; DB 2; Length 258;
Best Local Similarity 83.3%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTEHNGN 12
I:|||||
Db 131 CTYGVTHNGN 142

RESULT 11
A28664
enterotoxin A precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28664; A29566
R:Betley, M.J.; Mekalanos, J.J.
J. Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; MUID:88086892
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-references: GB:M18970; NID:9153120; PIDN:AAA26681.1; PID:9153121
A:Experimental source: strain FR1337
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; MUID:87222293
A:Accession: A29566
A:Molecule type: protein
A:Residues: 25-241, 'S', 243-257 <HUA>
C:Genetics:
A:Gene: entA
A:Map position: 6
C:Superfamily: enterotoxin B

Query Match 76.4%; Score 55; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 0.023;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
|||||
Db 130 CMYGVTLHDNN 141

RESULT 12
A28179
enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28179
R:Couch, J.L.; Solitis, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
A:Reference number: A28179; MUID:88257005
A:Accession: A28179
A:Molecule type: DNA
A:Residues: 1-257 <COU>
A:Cross-references: GB:M21319; NID:9153001; PIDN:AAA26617.1; PID:9153002
C:Superfamily: enterotoxin B

Query Match 76.4%; Score 55; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 0.023;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
|||||
Db 130 CMYGVTLHDNN 141

RESULT 13
B48826
high chorolytic hatching proteinase (EC 3.4.24.-) HCE23 precursor - Japanese medaka
C:Species: Oryzias latipes (Japanese medaka)
C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B48826
R:Yasumasu, S.; Yamada, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, D.
Dev. Biol. 153, 250-258, 1992
A:Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching
A:Reference number: A48826; MUID:93012471
A:Accession: B48826
A:Molecule type: mRNA
A:Residues: 1-270 <YAS>

A:Cross-references: GB:M96170; NID:9213501; PIDN:AAA49438.1; PID:9213502
A:Experimental source: orange red variety, embryo
A:Note: sequence extracted from NCBI backbone (NCBIN:114769, NCBIPI:114770)
A:Note: part of this sequence, including the amino end of the mature protein, was det
C:Superfamily: astacin; astacin homology
C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc
F:1-20/Domains: signal sequence #status predicted <SIG>
F:21-70/Domains: propeptide #status predicted <PRO>
F:71-270/Product: low chorolytic hatching proteinase #status predicted <MAT>
F:88-270/Domains: astacin homology <AST>
F:53/Binding site: carboxylate (Asn) (covalent) #status predicted
F:169,173,179,225/Binding site: zinc (His, His, Tyr) #status predicted
F:170/Active site: Glu #status predicted

Query Match 63.9%; Score 46; DB 2; Length 270;
Best Local Similarity 58.3%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
|||
Db 161 CMYGIQHHLN 172

RESULT 14
B48826
high chorolytic hatching proteinase (EC 3.4.24.-) HCE21 precursor - Japanese medaka
C:Species: Oryzias latipes (Japanese medaka)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 03-Dec-1999
C:Accession: B48826
R:Yasumasu, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, D.
Dev. Biol. 153, 250-258, 1992
A:Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching
A:Reference number: A48826; MUID:93012471
A:Accession: B48826
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-279 <YAS>
A:Cross-references: GB:M96171
C:Superfamily: astacin; astacin homology
C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc
F:1-20/Domains: signal sequence #status predicted <SIG>
F:21-79/Domains: propeptide #status predicted <PRO>
F:80-279/Product: low chorolytic hatching proteinase #status predicted <MAT>
F:97-279/Domains: astacin homology <AST>
F:62/Binding site: carboxylate (Asn) (covalent) #status predicted
F:178,182,188,234/Binding site: zinc (His, His, Tyr) #status predicted
F:179/Active site: Glu #status predicted

Query Match 63.9%; Score 46; DB 2; Length 279;
Best Local Similarity 58.3%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
|||
Db 170 CMYGIQHHLN 181

RESULT 15
T25259
hypothetical protein T25B9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T25259
R:Matthews, P.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z20006
A:Accession: T25259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-366 <MIL>
A:Cross-references: EMBL:Z70311; PIDN:CAA94374.1; GSPDB:GN00022; CESP:T25B9.2

A;Experimental source: clone T25B9

C;Genetics:

A;Gene: CESP:T25B9.2

A;Map position: 4

A;Intons: 66/3; 171/2; 239/3; 333/1

C;Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein

Query Match 62.5%; Score 45; DB 2; Length 366;
 Best Local Similarity 66.7%; Pred. No. 2.1;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMHGVTEH 9
 ||:|||||
 Db 199 CMHGVTEH 207

Search completed: January 2, 2002, 20:49:24
 Job time: 784 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:46:45 ; Search time 37.4 seconds

(without alignments)
11.764 Million cell updates/sec

Title: US-09-335-581a-3

Perfect score: 72

Sequence: 1 CMYGVTEHEGN 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	93.1	266	1 ETC1_STAUV	P01553 staphylococ
2	67	93.1	266	1 ETC2_STAUV	P34071 staphylococ
3	67	93.1	266	1 ETC3_STAUV	P23313 staphylococ
4	67	93.1	266	1 ETCB_STAUV	P01552 staphylococ
5	63	87.5	251	1 SPEA_STRPY	P08095 streptococ
6	60	83.3	258	1 ETCX_STAUV	P20723 staphylococ
7	55	76.4	257	1 ETCX_STAUV	P13163 staphylococ
8	55	76.4	257	1 ETCX_STAUV	P12993 staphylococ
9	46	63.9	270	1 HCE1_ORYLA	P31580 oryzias lat
10	46	63.9	279	1 HCE2_ORYLA	P31581 oryzias lat
11	41	56.9	150	1 YCCA_BACD3	P55815 bacillus ps
12	40	55.6	303	1 ROC_HUMAN	P07910 homo sapien
13	40	55.6	455	1 YSDI_CAELI	P48459 caenorhabdi
14	40	55.6	739	1 YG1Q_ECOLI	O46861 escherichia
15	40	55.6	877	1 AGLU_HORVU	O43763 hordeum vul
16	38	52.8	170	1 RS7_DESMO	P41206 desulfuroc
17	38	52.8	242	1 237A_HUMAN	P17032 homo sapien
18	38	52.8	437	1 ERRI_YEAST	P42222 saccharomyc
19	38	52.8	472	1 RE16_SCHPO	P40379 schizosacch
20	37	51.4	310	1 ASTL_COTJA	P46662 coturnix co
21	37	51.4	402	1 NK2R_CAVPO	O64077 cavia porce
22	37	51.4	413	1 HEMO_MANSE	P31398 manduca sex
23	37	51.4	466	1 SRM_MOUSE	O62270 mus musculu
24	37	51.4	523	1 DBP3_YEAST	P20447 saccharomyc
25	37	51.4	969	1 KBFI_HUMAN	P19838 homo sapien
26	37	51.4	971	1 KBFI_MOUSE	P23799 mus musculu
27	37	51.4	3635	1 LMA5_MOUSE	O61001 mus musculu
28	36.5	50.7	463	1 FTIB_CHICK	O02020 gallus gall
29	36	50.0	145	1 MOAE_HELPJ	O09144 heliobacte
30	36	50.0	169	1 PLMN_RAT	O01177 rattus norv
31	36	50.0	234	1 YP24_METTE	P29576 methanobact
32	36	50.0	237	1 YP24_METTE	P29575 methanobact
33	36	50.0	474	1 MEC3_YEAST	O02574 saccharomyc

ALIGNMENTS

34	36	50.0	775	1	TNP3_MOUSE	O60769 mus musculu
35	36	50.0	841	1	SECA_BACSU	P28366 bacillus su
36	36	50.0	842	1	IF2_TREPA	O93861 treponema p
37	36	50.0	908	1	CIC2_MOUSE	O97041 mus musculu
38	36	50.0	918	1	SCRA_LIMPO	O25390 limulus pol
39	36	50.0	1085	1	RBP2_BOVIN	P48820 bos taurus
40	36	50.0	1328	1	AGRI_DISOM	O90404 discopyge o
41	36	50.0	1955	1	AGRI_CHICK	P31696 gallus gall
42	36	50.0	3224	1	RBP2_HUMAN	P49792 homo sapien
43	35.5	49.3	1134	1	TIEL_MOUSE	O06806 mus musculu
44	35.5	49.3	1138	1	TIEL_HUMAN	P35590 homo sapien
45	35	48.6	134	1	YP96_MYCTU	O50625 mycobacteri

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RESULT 1
ETC1_STAUV STANDARD: PRT: 266 AA.
AC P01553:STAUV
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bonach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYROGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC -----
DR EMBL: X05815; GA29260.1; -
DR PIR: A01816; ENSAC1.
DR PIR: S06356; S06356.
DR HSSP: P34071.1SE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTR_TOXIN
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen.
FT CHAIN 1 27 ENTEROTOXIN TYPE C-1.
FT DISUFID 28 266
FT CONFLIT 177 177 D -> N (IN REF. 2).
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;

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Query Match 93.1%; Score 67; DB 1; Length 266;
 Best Local Similarity 83.3%; Pred. No. 6.9e-05;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMGCVTEHGN 12
 DB 137 CMGCVTEHGN 148

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RESULT 2
ETC3_STAU
ID ETC3_STAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ETC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bohach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2."
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96027099; PubMed=7582894;
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RA Brehm R.D., Tranter H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT Staphylococcus aureus reveals a zinc-binding site."
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F., Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RN [4]
RP Nat. Struct. Biol. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=9734373; PubMed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RN [5]
RP J. Mol. Biol. 269:270-280(1997).
RN [5]
RP DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1 SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC PIR: A60114; A60114.
CC PDB: 1STE; 23-DEC-96.
CC PDB: 1SE2; 08-MAR-96.
CC InterPro: IPR001961; Staph_Strep_toxin.
CC Pfam: PF01123; Staph_Strep_toxin; 1.
CC PRINTS: PR00279; BACTRTOXIN.
CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.
FT CHAIN 1 27
FT SIGNAL 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFID 120 137
FT METAL 36
FT METAL 110 ZINC.
FT METAL 145 ZINC.
FT METAL 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

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Query Match 93.1%; Score 67; DB 1; Length 266;
 Best Local Similarity 83.3%; Pred. No. 6.9e-05;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMGCVTEHGN 12
 DB 137 CMGCVTEHGN 148

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RESULT 3
ETC3_STAU
ID ETC3_STAU STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
GN ETC3.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90220508; PubMed=2325627;
RA Hoyde C.J., Hackett S.P., Bonach G.A.;
RT "Nucleotide sequence of all three type C staphylococcal
RT sequence comparison of all three type C staphylococcal
RT enterotoxins."
RN [2]
RP Mol. Gen. Genet. 220:329-333(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECEPTOR.
RX MEDLINE=97064178; PubMed=8906797;
RA Fields B.A., Malchiodi E.L., Li H., Ysern X., Stauffer C.V.,
RA Schlievert P.M., Karjalainen K., Marizaza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen."
RN [3]
RP Nature 384:188-192(1996).
RN [3]
RP DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1 SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC -----
CC EMBL: X51661; CAA35972.1; -.
CC PIR: S11885; S11885.
CC PDB: 1JCK; 12-NOV-97.
CC InterPro: IPR001961; Staph_Strep_toxin.
CC Pfam: PF01123; Staph_Strep_toxin; 1.
CC PRINTS: PR00279; BACTRTOXIN.
CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT CHAIN 1 27
FT SIGNAL 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137 BY SIMILARITY.
FT METAL 36
FT METAL 110 ZINC.
FT METAL 145 ZINC.
SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FFCA59 CRC64;

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Query Match 93.1%; Score 67; DB 1; Length 266;
 Best Local Similarity 83.3%; Pred. No. 6.9e-05;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMGCVTEHGN 12

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DB      137 CMYGGVTEHNGN 148
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RESULT  4
ETXB_STAAU STANDARD; PRT: 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE B PRECURSOR (SEB).
GN ENTB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus.";
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE=85298255; PubMed=3898073;
RA Raneill D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in
RT Escherichia coli and Staphylococcus aureus.";
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN [4]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyonogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence.";
RN [5]
RX J. Biol. Chem. 245:3518-3525(1970).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=93063291; PubMed=1436058;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RN [7]
RX Nature 359:801-806(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483;
RA Jardeatzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RT Chl Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RN [9]
RX Nature 368:711-718(1994).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=99096298; PubMed=9881971;
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
RT Karijainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RN [11]
RX Immunity 9:807-816(1998).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=96181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RN [13]
RX J. Mol. Biol. 277:61-79(1998).
RN [14]
RP -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
RN STAPHYLOCOCCAL FOOD POISONING SYNDROME.
RN [15]
RP -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
RN PYROGENIC EXOTOXINS ARE ALL RELATED.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M1118; AAA88550.1; -.
DR PIR; A01815; ENSAB6.
DR PIR; S27360; S27360.
DR PDB; 1SEB; 20-JUN-96.
DR PDB; 2SEB; 28-JAN-98.
DR PDB; 3SEB; 27-MAY-98.
DR PDB; 1SE3; 16-JUN-97.
DR PDB; 1SE4; 15-OCT-97.
DR PDB; 1SBB; 04-MAR-99.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTERIOTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE B.
FT DISULFD 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77 DDN -> NND (IN REF. 3).
FT CONFLICT 118 118 DQFLYFDLI -> NEFFDLIYL (IN REF. 3).
FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
FT CONFLICT 133 135 OTD -> ENT (IN REF. 3).
FT CONFLICT 149 150 NG -> GN (IN REF. 3).
FT CONFLICT 156 156 Y -> YV (IN REF. 3).
FT CONFLICT 156 156 D -> EQ (IN REF. 3).
FT CONFLICT 185 186 OE -> EQ (IN REF. 3).
FT CONFLICT 233 233 D -> N (IN REF. 3).
FT CONFLICT 246 247 DN -> ND (IN REF. 3).
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CFO18B0 CMC64;
Query Match 93.1%; Score 67; DB 1; Length 266;
Best Local Similarity 91.7%; Pred. No. 6.9e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CMYGGVTEHNGN 12
DB 140 CMYGGVTEHNGN 151
RESULT 5
SPEA_STRPY STANDARD; PRT: 251 AA.
AC P068095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
DE (SFE A).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
CC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12.";
RN [2]
RX Infect. Immun. 52:144-150(1986).
RN [3]
RP SEQUENCE FROM N.A.

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OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FR137;
 RX MEDLINE=88086892; PubMed=3335483;
 RA Boley M.J., Mekalanos J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene";
 RL J. Bacteriol. 170:34-41(1988).
 RN [2]
 RP SEQUENCE OF 25-257.
 RX MEDLINE=87222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A";
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354648; PubMed=7628431;
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlstien M., Kalland T.,
 RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
 RT "Crystal structure of the superantigen staphylococcal enterotoxin
 type A";
 RL EMBO J. 14:3292-3301(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278;
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlstien M.,
 RA Abrahamson L.;
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 Zn²⁺ at 2.7-A resolution. Implications for major histocompatibility
 complex class II binding.";
 RL J. Biol. Chem. 271:3212-3221(1996).
 RN [5]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [6]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- SUBUNIT: MONOMER.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
 PROGENIC EXOTOXINS ARE ALL RELATED.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M18970; AAA26681.1; -
 DR PIR; A28664; A28664.
 DR PIR; A29566; A29566.
 DR PDB; 1ESE; 11-JUL-96.
 DR PDB; 1SEA; 15-OCT-95.
 DR PDB; 1SXT; 19-NOV-97.
 DR InterPro; IPR001961; Staph_Strep_toxin.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRTOXIN.

DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISULFID 120 130
 FT METAL 25 25 ZINC.
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T->S (IN REF. 2).
 SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCA1F14677 CRC64;
 Query Match 76.4%; Score 55; DB 1; Length 257;
 Best Local Similarity 75.0%; Pred. NO. 0.0097;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CMYGVTEHEGN 12
 Db 130 CMYGVTLHDNN 141
 RESULT 8
 ETYPE STAAU STANDARD; PRT: 257 AA.
 ID ETYPE STAAU STANDARD; PRT: 257 AA.
 AC P12993;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
 GN ENTE.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC STRAIN=MJB265;
 RX MEDLINE=88257005; PubMed=3384800;
 RA Couch J.L., Solits M.T., Boley M.J.;
 RT "Cloning and nucleotide sequence of the type E staphylococcal
 enterotoxin gene";
 RL J. Bacteriol. 170:2954-2960(1988).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins";
 RL Nat. Struct. Biol. 2:680-686(1995).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
 PROGENIC EXOTOXINS ARE ALL RELATED.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M21319; AAA26617.1; -
 DR PIR; A28179; A28179.
 DR PDB; 1SEE; 15-OCT-95.
 DR InterPro; IPR001961; Staph_Strep_toxin.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.

FT SIGNAL 1 27
 FT CHAIN 28 257 ENTEROTOXIN TYPE E.
 SQ SEQUENCE 257 AA: 29358 MM; 27EDA9AB97770CE3 CRC64;

Query Match 76.4%; Score 55; DB 1; Length 257;
 Best Local Similarity 75.0%; Pred. No. 0.0097;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
 DB 130 CMYGVTLHDNN 141

RESULT 9
 HCEL_ORYLA STANDARD; PRT: 270 AA.
 AC P31580;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HIGH CHORIOLYTIC ENZYME 1 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME
 DE ZINC-PROTEASE HCE 1 SUBUNIT) (CHORIOLYSIN H 1).
 GN HCE 23.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adriantichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 71-119 AND 208-223.
 RC TISSUE=embryo;
 RX MEDLINE=93012471; PubMed=1397682;
 RA Yasumasa S., Yamada K., Akasaka K., Mitsuana K., Iuchi I.,
 RA Shimada H., Yamagami K.;
 RT *Isolation of cDNAs for LCE and HCE, two constituent proteases of the
 RT hatching enzyme of Oryzias latipes, and concurrent expression of the
 RT their mRNAs during development.*;
 RL Dev. Biol. 153:250-258(1992).
 CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,
 CC WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME
 CC OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.
 CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE
 CC CHORIOLYTIC SMELLING ACTION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG
 CC ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES
 CC SUCH AS SUC-LEU-LEU-VAL-TYR-I-MCA.
 CC -1- COFACTOR: BINDS ONE ZINC ION.
 CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZYMOGEN
 CC GRANULES.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY
 CC 2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.
 CC -1- PTM: O-GLYCOSYLATED (PROBABLY).
 CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF
 CC TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE), OF
 CC WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME
 CC (LCE).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
 CC METALLOPROTEASE); ALSO KNOWN AS THE ASPACIN SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M96170; AAA43438.1; -
 CC DR PIR: B48826; B48826.
 CC DR HSSP: P07584; 11AD.
 CC DR MEROPS: M12.007; -.

DR InterPro: IPR001506; Astacin.
 DR InterPro: IPR000130; Zn_Mrpeptidse.
 DR Pfam: PF01400; Astacin.1.
 DR PRINTS: PR00480; ASTACIN.
 DR SMART: SM00235; zmc.1.
 DR PROSITE: PS00142; ZINC-PROTEASE; 1.
 DR Hydrolyase; Metalloprotease; Zinc; Glycoprotein; Zymogen; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 70 ACTIVATION PEPTIDE.
 FT CHAIN 71 270 HIGH CHORIOLYTIC ENZYME 1.
 FT METAL 169 169 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 170 170 BY SIMILARITY.
 FT METAL 173 173 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 270 AA; 30392 MM; D85C972906E3735A CRC64;

Query Match 63.9%; Score 46; DB 1; Length 270;
 Best Local Similarity 58.3%; Pred. No. 0.43;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
 DB 161 CMYSLIIGHN 172

RESULT 10
 HCE2_ORYLA STANDARD; PRT: 279 AA.
 AC P31581;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HIGH CHORIOLYTIC ENZYME 2 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME
 DE ZINC-PROTEASE HCE 2 SUBUNIT) (CHORIOLYSIN H 2).
 GN HCE 21.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adriantichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RX MEDLINE=93012471; PubMed=1397682;
 RA Yasumasa S., Yamada K., Akasaka K., Mitsuana K., Iuchi I.,
 RA Shimada H., Yamagami K.;
 RT *Isolation of cDNAs for LCE and HCE, two constituent proteases of the
 RT hatching enzyme of Oryzias latipes, and concurrent expression of
 RT their mRNAs during development.*;
 RL Dev. Biol. 153:250-258(1992).
 CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,
 CC WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME
 CC OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.
 CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE
 CC CHORIOLYTIC SMELLING ACTION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG
 CC ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES
 CC SUCH AS SUC-LEU-LEU-VAL-TYR-I-MCA.
 CC -1- COFACTOR: BINDS ONE ZINC ION.
 CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZYMOGEN
 CC GRANULES.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY
 CC 2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.
 CC -1- PTM: O-GLYCOSYLATED (PROBABLY).
 CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF
 CC TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE), OF
 CC WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME
 CC (LCE).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
 CC METALLOPROTEASE); ALSO KNOWN AS THE ASPACIN SUBFAMILY.
 CC -----

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CC EMBL: M6171; AAA9439.1; -
CC HSSP: P07584; 11AD.
CC MEROPS: M12.007; -
CC InterPro: IPR001506; Astacin.
CC InterPro: IPR000130; Zn.MTpeptidase.
CC Pfam: PF01400; Astacin.1.
CC PRINTS: PRO0480; ASTACIN.
CC SMART: SM00235; Zmnc.1.
CC PROSITE: PS00142; ZINC_1-PROTEINASE; 1.
CC Hydrolase: Metalloproteinase; Zinc; Glycoprotein; Zymogen; Signal.
CC FT SIGNAL 1 20
CC FT PROPEP 21 79 ACTIVATION PEPTIDE.
CC FT CHAIN 80 279 HIGH CHORIOLYTIC ENZYME 2.
CC FT METAL 178 178 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT ACT_SITE 179 179 BY SIMILARITY.
CC FT METAL 182 182 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT METAL 188 188 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 279 AA; 31490 MW; 00244107AB801B8C CRC64;

OY 1 CMYGVTEHGN 12
Db 170 CMYSGI0HELN 181

RESULT 11
ID YCCA_BACP3 STANDARD; PRT; 150 AA.
AC P55815;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHEICAL PROTEIN IN CCA 5' REGION (FRAGMENT).
OS Bacillus PS3 (Thermophilic bacterium PS-3).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=70306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93379042; PubMed=7916623;
RA Fujiwara Y., Oka M., Hamamoto T., Sone N.;
RT "Cytochrome c-551 of the thermophilic bacterium PS3, DNA sequence and
RT analysis of the mature cytochrome.";
RL Biochem. Biophys. Acta 1144:213-219(1993).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: TO B.SUBTILIS VPJC, YOFU AND YITF.

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CC EMBL: X6125; -; NOT_ANNOTATED_CDS.
CC KW Hypothetical protein; Transmembrane.
CC NON_TER 1 1
CC TRANSMEM 19 39 POTENTIAL.

SQ SEQUENCE 150 AA; 16394 MW; AEF6892DB2CF7447 CRC64;

OY 3 YGVTEH 10
Db 99 YGVTEH 106

RESULT 12
ROC_HUMAN
ID ROC_HUMAN STANDARD; PRT; 303 AA.
AC P07910; P22628;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 / HNRNP C2).
GN HNRPC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90099350; PubMed=2557628;
RA Burd C.G., Swanson M.S., Goerlach M., Dreyfuss G.;
RT "Primary structures of the heterogeneous nuclear ribonucleoprotein
RT A2, B1, and C2 proteins: a diversity of RNA binding proteins is
RT generated by small peptide inserts";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9788-9792(1989).
RN [2]
RP SEQUENCE OF 1-107 AND 121-303 FROM N.A.
RX MEDLINE=87257872; PubMed=3110598;
RA Swanson M.S., Nakagawa T.Y., Levan K., Dreyfuss G.;
RT "Primary structure of human nuclear ribonucleoprotein particle C
RT proteins: conservation of sequence and domain structures in
RT heterogeneous nuclear RNA, mRNA, and pre-rRNA-binding proteins.";
RL Mol. Cell. Biol. 7:1731-1739(1987).
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=90067819; PubMed=2587210;
RA Merrill B.M., Barnett S.F., Lestourgeon W.M., Williams K.R.;
RT "Primary structure differences between proteins C1 and C2 of HeLa 40S
RT nuclear ribonucleoprotein particles.";
RL Nucleic Acids Res. 17:8441-8449(1989).
RN [4]
RP STRUCTURE BY NMR OF 1-94.
RX MEDLINE=92329450; PubMed=1385725;
RA Witteking M., Goerlach M., Friedrichs M., Dreyfuss G., Mueller L.;
RT "1H, 13C, and 15N NMR assignments and global folding pattern of the
RT RNA-binding domain of the human hnrnp C proteins.";
RL Biochemistry 31:6254-6265(1992).
RN [5]
RP STRUCTURE BY NMR OF 1-94.
RX MEDLINE=92371436; PubMed=1380452;
RA Goerlach M., Witteking M., Beckman R.A., Mueller L., Dreyfuss G.;
RT "Interaction of the RNA-binding domain of the hnrnp C proteins with
RT RNA.";
RL EMBO J. 11:3289-3295(1992).
CC -1- FUNCTION: MAY PLAY A ROLE IN RIBONUCLEOSOME ASSEMBLY BY
CC NEUTRALIZING BASIC PROTEINS SUCH AS A AND B CORE HNRNP.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; COMPONENT OF RIBONUCLEOSOMES.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; C1 AND C2 (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- PMW: PHOSPHORYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).

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 CC -----
 DR EMBL: M29063; AAA36576.1; -
 DR EMBL: M16342; AAA52680.1; -
 DR PIR: G34504; C34504.
 DR PIR: A26885; A26885.
 DR SWISS-2DPAGE: P07910; HUMAN.
 DR Aarhus/Ghent-2DPAGE: 7207; IEF.
 DR Aarhus/Ghent-2DPAGE: 7222; IEF.
 DR MIM: 164020;
 DR InterPro: IPR000504; RRM.
 DR Pfam: PF00076; Irm; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS50102; RRM; 1.
 DR PROSITE: PS00030; RRM_RNP_1; 1.
 DR Nuclear protein; RNA-binding; Ribonucleoprotein; Phosphorylation;
 KW Alternative splicing.
 FT DOMAIN 16 87 RNA-BINDING (RRM).
 FT DOMAIN 155 161 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 181 303 ASP/GLU-RICH (ACIDIC).
 FT VARSPLIC 108 120 MISSING (IN ISOPFORM HNRP C1).
 SQ SEQUENCE 303 AA; 33298 MW; E1B08298184AAC46 CRC64;

Query Match 55.6%; Score 40; DB 1; Length 303;
 Best Local Similarity 87.5%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MYGVTEH 9
 DB 104 MYGVTEH 111

RESULT 13
 YSD1_CAEEL STANDARD; PRT; 455 AA.
 AC P48459;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C23G10.1 IN CHROMOSOME
 DE II (RC 3.1.3.16).
 GN C23G10.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Latreille P.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases
 CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H2O -> A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-1
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: U39851; AAA81073.1; -
 DR HSSP: P08129; IFTM.
 DR Wormpep: C23G10.1; CE01808.
 DR InterPro: IPR000934; Ser-thc_phosphatse.
 DR InterPro: IPR001394; UCH-2.

DR Pfam: PF00149; STphosphatase; 1.
 DR Pfam: PF00442; UCH-1; 1.
 DR PRINTS: PR00114; STPHPTASE.
 DR SMART: SM00156; PP2AC; 1.
 DR PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.
 KW Hypothetical protein; Hydrolase; Iron; Manganese.
 FT METAL 191 191 IRON (BY SIMILARITY).
 FT METAL 193 193 IRON (BY SIMILARITY).
 FT METAL 221 221 IRON AND MANGANESE (BY SIMILARITY).
 FT METAL 253 253 MANGANESE (BY SIMILARITY).
 FT ACT_SITE 254 254 GENERAL ACID (BY SIMILARITY).
 FT METAL 305 305 MANGANESE (BY SIMILARITY).
 FT METAL 379 379 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 455 AA; 51837 MW; BEB5A1A94FFEBB CRC64;

Query Match 55.6%; Score 40; DB 1; Length 455;
 Best Local Similarity 55.6%; Pred. No. 8.7;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEH 9
 DB 303 CMYGVTEH 311

RESULT 14
 YG10_ECOLI STANDARD; PRT; 739 AA.
 AC Q46861; Q46862;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 83.5 KDA PROTEIN IN METC-SUFI INTERGENIC REGION.
 GN YG10 OR B3015/B3016.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=9742617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP CONCEPTUAL TRANSLATION.
 RC Rudd K.E.;
 RL Unpublished observations (JUN-1999).
 CC -1- SIMILARITY: TO M. JANNASCHII MJ1155. ALSO SOME SIMILARITY TO FAMILY
 CC UPF0004.
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
 CC INTRODUCED IN POSITION 319 TO PRODUCE THIS ORF.
 CC -----
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 CC -----
 DR EMBL: U28377; AA69183.1; ALT_FRAME.
 DR EMBL: U28377; AA69184.1; ALT_FRAME.
 DR EMBL: AE000383; AAC76052.1; ALT_FRAME.
 DR EMBL: AE000383; AAC76051.1; ALT_FRAME.
 DR Ecogene: EG13019; YG10.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 739 AA; 83503 MW; ECE565EC8915384A CRC64;

Query Match 55.68; Score 40; DB 1; Length 729;
Best Local Similarity 54.58; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CMYGVTEHEG 11
1 : |||||
Db 390 CSFCSITEHEG 400

|||||:1
Db 481 YGVTEYE 488

Search completed: January 2, 2002, 20:50:15
Job time: 210 sec

RESULT 15
AGLU_HORVU STANDARD; PRT; 877 AA.
AC 043763;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA-GLUCOSIDASE PRECURSOR (EC 3.2.1.20) (MALTASE).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triliceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MOREX; TISSUE=Aleurone;
RX MEDLINE=96178863; Pubmed=9616248;
RA Tibbot B.K., Skadsen R.W.;
RT "Molecular cloning and characterization of a gibberellin-inducible,
RT putative alpha-glucosidase gene from barley.";
RL Plant Mol. Biol. 30:229-241(1996).
CC -1 CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING
CC 1,4-LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.
CC -1 TISSUE SPECIFICITY: HIGH LEVELS SEEN IN THE ALEURONE AND SCUTELLUM
CC AFTER GERMINATION, WHILE LOW LEVELS ARE FOUND IN DEVELOPING SEEDS.
CC -1 DEVELOPMENTAL STAGE: LEVELS INCREASE STEADILY THROUGHOUT
CC IMBIBITION REACHING MAXIMUM LEVELS AT DAY 7. DURING GERMINATION,
CC LEVELS INCREASE FROM DAY 2, REACH MAXIMUM LEVELS AT DAY 3 AND
CC DECLINE AFTER DAY 5.
CC -1 INDUCTION: BY GIBBERELLIN A3 (GA).
CC -1 SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL: U22450; AAB02985.1; -
DR InterPro: IPR000322; Glyco_hydro_31.
DR Pfam: PF01055; Glyco_hydro_31; 1.
DR PROSITE: PS00129; GLYCOSYL_HYDROL_F31_1; 1.
DR PROSITE: PS00707; GLYCOSYL_HYDROL_F31_2; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 877 ALPHA-GLUCOSIDASE.
FT ACT_SITE 437 437 BY SIMILARITY.
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 877 AA; 96933 MW; E3B5C16E4588C492 CRC64;

Query Match 55.68; Score 40; DB 1; Length 877;
Best Local Similarity 87.58; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 YGVTEHE 10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:48:15 ; Search time 92.66 Seconds
(Without alignments)
18.943 Million cell updates/sec

Title: US-09-335-581a-3
Perfect score: 72
Sequence: 1 CMYGVTEHGN 12

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_protent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	95.8	136	2 099T49	099T49 staphylococ
2	67	93.1	234	2 09R5X4	09R5X4 staphylococ
3	67	93.1	239	2 005157	005157 staphylococ
4	67	93.1	239	2 005678	005678 staphylococ
5	67	93.1	239	2 006531	006531 staphylococ
6	67	93.1	239	2 006532	006532 staphylococ
7	67	93.1	239	2 006533	006533 staphylococ
8	67	93.1	239	2 006534	006534 staphylococ
9	67	93.1	239	2 006535	006535 staphylococ
10	67	93.1	271	2 09F0L6	09F0L6 staphylococ
11	63	87.5	222	2 09S5Z4	09S5Z4 streptococ
12	63	87.5	222	2 09R931	09R931 streptococ
13	63	87.5	236	2 054696	054696 streptococ
14	63	87.5	236	2 054779	054779 streptococ
15	63	87.5	236	2 057453	057453 streptococ
16	63	87.5	236	2 057163	057163 streptococ
17	60	83.3	179	2 052075	052075 plasmid p1b
18	59	81.9	260	2 054738	054738 streptococ
19	59	81.9	260	2 054971	054971 streptococ

20	59	81.9	260	2 054739	054739 streptococ
21	58	80.6	258	2 09EZM4	09EZM4 staphylococ
22	58	80.6	268	2 085217	085217 staphylococ
23	55	76.4	260	2 099SU3	099SU3 staphylococ
24	54	75.0	260	2 099T46	099T46 staphylococ
25	54	75.0	261	2 09EZM8	09EZM8 staphylococ
26	46	63.9	266	13 013116	013116 oryzias lat
27	45	62.5	366	5 027528	027528 caenorhabd1
28	45	62.5	375	5 09XW33	09XW33 caenorhabd1
29	43	59.7	347	4 09NM14	09NM14 homo sapien
30	43	59.7	1266	4 09NTE6	09NTE6 homo sapien
31	43	59.7	1353	4 09BY58	09BY58 homo sapien
32	42	58.3	203	10 065135	065135 lycopersico
33	41	56.9	366	2 09AAC7	09AAC7 caulobacter
34	41	56.9	644	10 023460	023460 arabidopsis
35	41	56.9	664	10 09ZM39	09ZM39 arabidopsis
36	41	56.9	669	10 09ZM30	09ZM30 arabidopsis
37	41	56.9	690	10 09L1B7	09L1B7 arabidopsis
38	40	55.6	156	2 09ABR6	09ABR6 caulobacter
39	40	55.6	157	2 099P7	099P7 staphylococ
40	40	55.6	347	2 09XAN5	09XAN5 streptomyce
41	40	55.6	354	11 09J1S1	09J1S1 mus musculu
42	40	55.6	367	5 09NAP8	09NAP8 caenorhabd1
43	40	55.6	373	11 09QYV1	09QYV1 rattus norv
44	40	55.6	380	4 013086	013086 homo sapien
45	40	55.6	388	10 09STX2	09STX2 arabidopsis

ALIGNMENTS

RESULT 1
ID 099T49 PRELIMINARY; PRT; 136 AA.
AC 099T49;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENTEROTOXIN YENT2.
CN YENT2 OR SA1644.
OS Staphylococcus aureus subsp. aureus N315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
CX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuoda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kohara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant staphylococcus
aureus."
RT Lancet 357:1225-1240(2001).
RL EMBL: AP003135; BAB42912.1; .
KW Complete proteome.
SQ SEQUENCE 136 AA; 15945 MW; D7C6C19820C45FE CRC64;

Query Match 95.8%; Score 69; DB 2; Length 136;
Best Local Similarity 91.7%; Pred. No. 4.7e-05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTEHGN 12
|||||
Db 5 CMYGVTEHGN 16
|||||
RESULT 2
09R5X4 PRELIMINARY; PRT; 234 AA.
ID 09R5X4

AC Q095X4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN-PYROGENIC TOXIN.
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group.
OX NCBI_Taxid=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9432595; Pubmed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP; P34071; 1SE2.
DR InterPro: IPR001961; Staph.Strep.toxin.
DR Pfam: PF01123; Staph.Strep.toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 93.18; Score 67; DB 2; Length 234;
Best Local Similarity 83.38; Pred. No. 0.00021;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
|||||:|||||
Db. 105 CMYGVTEHGN 116

RESULT 3
ID- 005157 PRELIMINARY; PRT; 239 AA.
AC 005157;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE C ENTEROTOXIN (FRAGMENT).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_Taxid=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Derlinger J.R., Callantine S.D., Dechald C.F.,
RL Berger P.H., Kapur V., Straufacher C.V., Bohach G.A.;
Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; 1JCK.
DR InterPro: IPR001961; Staph.Strep.toxin.
DR Pfam: PF01123; Staph.Strep.toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27536 MW; D66064460DE4191 CRC64;

Query Match 93.18; Score 67; DB 2; Length 239;
Best Local Similarity 83.38; Pred. No. 0.00021;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
|||||:|||||
Db. 110 CMYGVTEHGN 121

RESULT 4
O53678 PRELIMINARY; PRT; 239 AA.
ID Q53678

AC Q053678;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; Pubmed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro: IPR001961; Staph.Strep.toxin.
DR Pfam: PF01123; Staph.Strep.toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 93.18; Score 67; DB 2; Length 239;
Best Local Similarity 83.38; Pred. No. 0.00021;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
|||||:|||||
Db. 110 CMYGVTEHGN 121

RESULT 5
ID- 006531 PRELIMINARY; PRT; 239 AA.
AC 006531;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
RX MEDLINE=94011313; Pubmed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro: IPR001961; Staph.Strep.toxin.
DR Pfam: PF01123; Staph.Strep.toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00021;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
DB 110 CMYGVTEHGN 121

RESULT 6
ID 006532 PRELIMINARY; PRT; 239 AA.
AC 006532;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DE 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
EMBL: L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00021;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
DB 110 CMYGVTEHGN 121

RESULT 7
ID 006533 PRELIMINARY; PRT; 239 AA.
AC 006533;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DE 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCOCPELAND;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";

RL Infect. Immun. 61:4254-4262(1993).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
EMBL: L13378; AAA26622.1; -.
DR HSSP; P34071; 1STE.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00021;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
DB 110 CMYGVTEHGN 121

RESULT 8
ID 006534 PRELIMINARY; PRT; 239 AA.
AC 006534;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DE 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
EMBL: L13379; AAA26623.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00021;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
DB 110 CMYGVTEHGN 121

RESULT 9
ID 006535 PRELIMINARY; PRT; 239 AA.

AC 006535;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRI 909;
 RA MEDLINE=94011313; PubMed=8406814;
 RA Mair J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications.";
 RL Infect. Immun. 61:4254-4262(1993)
 CC -I- DISASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYROGENIC EXOTOXINS ARE ALL RELATED.
 CC EMBL: L13377; AAA26621.1; -
 DR HSSP: P23313; 1JCK.
 DR InterPro: IPR001961; Staph_Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin.1.
 DR PRINTS: PR00279; BACTR1TOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Superantigen.
 FT NON_TER 1
 SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E119E0 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 239;
 Best Local Similarity 83.3%; Pred. No. 0.00021;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CMYGVTEHGN 12
 DB 110 CMYGVTEHGN 121

RESULT 10
 ID 09F0L6 PRELIMINARY; PRT; 271 AA.
 AC 09F0L6.
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE STAPHYLOCOCCAL ENTEROTOXIN C-BOVINE.
 GN SEC-BOV.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=2056666; PubMed=11114901;
 RA FitzGerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
 RA Meaney W.J., Smyth C.J.;
 RT "Characterization of a putative pathogenicity island from bovine
 RT Staphylococcus aureus encoding multiple superantigens.";
 RL J. Bacteriol. 183:63-70(2001).
 CC EMBL: AF217235; AAG29599.1;
 DR InterPro: IPR001961; Staph_Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin.1.
 DR PRINTS: PR00279; BACTR1TOXIN.
 SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 93.1%; Score 67; DB 2; Length 271;
 Best Local Similarity 83.3%; Pred. No. 0.00024;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
 DB 142 CMYGVTEHGN 153

RESULT 11
 ID 09S5Z4 PRELIMINARY; PRT; 222 AA.
 AC 09S5Z4.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE EXOTOXIN TYPE A (FRAGMENT).
 GN SP6A.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D633;
 RA Bessen D.E., Izso M.W., Fiorentino T.R., Carling R.M., Beall B.;
 RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
 RT tropisms in group A streptococci.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF029051; AAD21315.1; -
 DR HSSP: P08095; 1B1Z.
 DR InterPro: IPR001961; Staph_Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin.1.
 DR PRINTS: PR00279; BACTR1TOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 222 AA; 25884 MW; 121F846092818F8 CRC64;

Query Match 87.5%; Score 63; DB 2; Length 222;
 Best Local Similarity 83.3%; Pred. No. 0.001;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHGN 12
 DB 108 CMYGVTEHGN 119

RESULT 12
 ID 09R931 PRELIMINARY; PRT; 222 AA.
 AC 09R931.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE EXOTOXIN A (FRAGMENT).
 GN SP6A.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D709;
 RA Bessen D.E., Izso M.W., Fiorentino T.R., Carling R.M.,
 RA Hollingshead S.K., Beall B.;
 RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
 RT tropism in group A streptococci.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF055698; AAD11624.1; -
 DR HSSP: P08095; 1B1Z.
 DR InterPro: IPR001961; Staph_Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin.1.
 DR PRINTS: PR00279; BACTR1TOXIN.

```
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match
Best Local Similarity 87.5%; Score 63; DB 2; Length 222;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
Db 108 CIYGVTHNEGN 119

RESULT 13
O54696 PRELIMINARY; PRT; 236 AA.
AC O54696;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
EMBL; X61573; CAA43771.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match
Best Local Similarity 87.5%; Score 63; DB 2; Length 236;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
Db 120 CIYGVTHNEGN 131

RESULT 14
O54779 PRELIMINARY; PRT; 236 AA.
AC O54779; O54613; O54736; O54740; O54741;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
```

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OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
EMBL; X61569; CAA43767.1; -.
DR EMBL; X61572; CAA43770.1; -.
DR EMBL; X61568; CAA43766.1; -.
DR EMBL; X61570; CAA43768.1; -.
DR EMBL; X61571; CAA43769.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match
Best Local Similarity 87.5%; Score 63; DB 2; Length 236;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTEHEGN 12
Db 120 CIYGVTHNEGN 131

RESULT 15
O57453 PRELIMINARY; PRT; 236 AA.
AC O57453;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS496;
MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
EMBL; X61563; CAA43760.1; -.
DR EMBL; X61567; CAA43761.1; -.
DR EMBL; X61567; CAA43765.1; -.
DR EMBL; X61561; CAA43759.1; -.
DR EMBL; X61564; CAA43762.1; -.
DR EMBL; X61565; CAA43763.1; -.
DR EMBL; X61566; CAA43764.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
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DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 22 POTENTIAL.
 FT CHAIN 23 >236 TYPE A EXOTOXIN.
 FT NON_TER 236 236
 SQ SEQUENCE 236 AA: 27484 MW: 2EF7F41AAC853600 CRC64;

Query Match 87.5%; Score 63; DB 2; Length 236;
 Best Local Similarity 83.3%; Pred. No. 0.0011;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTEHEGN 12
 1:1111111111
 Db 120 CIYGGVTNHEGN 131

Search completed: January 2, 2002, 20:52:02
 Job time: 227 sec

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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:48:13 ; Search time 77.31 Seconds
(without alignments)
11.498 Million cell updates/sec

Title: US-09-335-581A-34
Perfect score: 71
Sequence: 1 CMWGVTLHEGN 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
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20: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	90.1	12	19	AAW72422
2	64	90.1	12	21	AAV97836
3	64	90.1	12	21	AAV97846
4	64	90.1	12	22	AAV72176
5	64	90.1	12	22	AAV72184
6	64	90.1	14	19	AAW72424
7	64	90.1	14	21	AAV97840
8	64	90.1	14	22	AAV72178
9	64	90.1	36	19	AAW72426
10	64	90.1	36	21	AAV97842
11	64	90.1	36	22	AAV72180

12	64	90.1	38	19	AAW72427	Peptide #6 for red
13	64	90.1	38	21	AAV97843	Staphylococcal/str
14	64	90.1	38	22	AAV72181	Peptide #6348, der
15	64	90.1	238	12	AAK13208	Staphylococcal ent
16	64	90.1	238	14	AAK45016	Staphylococcal ent
17	64	90.1	238	22	AAK67343	Staphylococcal ent
18	64	90.1	239	12	AAK13207	Staphylococcal ent
19	64	90.1	239	14	AAK45015	Staphylococcal ent
20	64	90.1	239	20	AAV06254	Staphylococcal gro
21	64	90.1	239	20	AAV06255	Staphylococcal gro
22	64	90.1	239	20	AAV06256	Staphylococcal gro
23	64	90.1	239	20	AAV06257	Staphylococcal gro
24	64	90.1	239	20	AAV06258	Staphylococcal gro
25	64	90.1	239	20	AAV06251	Staphylococcal gro
26	64	90.1	239	20	AAV06252	Staphylococcal gro
27	64	90.1	239	20	AAV06253	Staphylococcal gro
28	64	90.1	239	22	AAK67342	Staphylococcal ent
29	64	90.1	266	21	AAV70108	Staphylococcal ent
30	62	87.3	12	21	AAV97844	Staphylococcal ent
31	62	87.3	12	21	AAV97848	Staphylococcal ent
32	62	87.3	12	22	AAV72182	Peptide from regio
33	62	87.3	12	22	AAV72186	Peptide from regio
34	62	87.3	23	17	AAW04492	Staphylococcal ent
35	62	87.3	23	20	AAW73919	Staphylococcal ent
36	62	87.3	230	12	AAK13204	Staphylococcal ent
37	62	87.3	230	14	AAK45012	Staphylococcal ent
38	62	87.3	230	22	AAK67339	Staphylococcal ent
39	62	87.3	233	12	AAK13203	Staphylococcal ent
40	62	87.3	233	18	AAK45011	Staphylococcal ent
41	62	87.3	233	18	AAK35373	Staphylococcal ent
42	62	87.3	233	18	AAW06738	Staphylococcal ent
43	62	87.3	233	21	AAV70103	Mutant Staphylococ
44	62	87.3	233	21	AAV54463	Amino acid sequenc
45	62	87.3	233	22	AAK67338	Staphylococcus aur

ALIGNMENTS

RESULT 1
ID AAW72422 standard; peptide: 12 AA.
XX
AC AAW72422;
XX
DT 22-DEC-1998 (first entry)
XX
DE Peptide #1 for reducing symptoms of toxic shock syndrome.
XX
KW Toxic shock syndrome; immunogenic response; bacterial infection;
KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
KW autoimmune disease.
XX
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
XX
PN W09845325-A1.
XX
PD 15-OCT-1998.
PD
PF 01-APR-1998; 98WO-US06663.
PF
PR 07-APR-1997; 97US-0838413.
PR
PA (UYRQ) UNTV ROCKEFELLER.
PA
PI Bannan JD, Zabriskie JB;
PI
DR WPI: 1998-568335/48.
XX
PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic

PT shock and autoimmune diseases
XX
PS Claim 4; Page 53; 69pp; English.
XX
CC The present invention describes peptides having consensus sequences #1
CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
CC Where consensus sequence #1 and #2 are: X25X26YGX17X23X4X3N #1,
CC K66X78X9X10X11X12X13DX14X15X16RX17X18X20X21X22X23X24Y #2, where
CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
CC or are absent; X27 = L or Y; all other x may be any aa. The peptides
CC can be used to generate serum antibodies (Ab) that bind at least one
CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
CC cells in presence of these toxins (i.e. to protect against or alleviate
CC toxic shock or autoimmune disease associated with bacterial infections);
CC and (iii) for passive immunisation against effects of the toxins. The
CC peptides generate Ab that are cross-reactive with toxins from a variety
CC of bacteria. The present sequence represents a specifically claimed
CC example of a peptide of the present invention.
XX
SQ Sequence 12 AA:
Query Match 90.1%; Score 64; DB 19; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CMYGVTLHEGN 12
Db 1 CMYGVTEHEGN 12
IIIIIIIIII
RESULT 2
AAV97838
ID AAV97838 standard; peptide: 12 AA.
XX
AC AAV97838;
XX
DT 29-AUG-2000 (first entry)
XX
DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6343.
XX
KM Pyrogenic exotoxin; enterotoxin; streptococcal infection;
XX staphylococcal infection; septic shock; toxic shock; vaccine;
XX antibody.
OS Synthetic.
OS Staphylococcus aureus.
OS Streptococcus sp. 'Group A'.
XX
PN MO200020598-A1.
XX
PD 13-APR-2000.
XX
PF 24-SEP-1999; 99WO-US22180.
XX
PR 07-OCT-1998; 98US-0168303.
PR 18-JUN-1999; 99US-0335581.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Bannan JD, Visvanathan K, Zabriskie JB;
XX
DR WPI; 2000-303782/26.
XX
PT Peptides useful for preventing and reducing the symptoms of toxic shock
PT syndrome and septic shock from staphylococcal and streptococcal
PT infections -
XX
PS Claim 4; Page 88; 115pp; English.
XX
CC The invention relates to novel peptides (AAV97838-Y97843) comprising a

CC consensus amino acid sequence derived from two conserved regions
CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
CC consensus region 1) has the sequence X25-X26-Y-G-X1-T-X2-X3-X4-X5-N
CC (AAV97863) and consensus region 2a (a preferred consensus region 2) has
CC the sequence K-X6-X7-X8-
CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
CC (AAV97864), where: X1, X8, X13 and X24 are each independently selected
CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
CC the group consisting of any amino acid;
CC X3, X5 and X26 are each independently selected from the group consisting
CC of any amino acid and of no amino acid;
CC X27 is either L or Y.
CC The invention also relates to serum antibodies induced by the peptides
CC which provide protection against, or reduce the severity of toxic shock
CC and septic shock caused by the staphylococcal and streptococcal
CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic
CC exotoxins) constitute a family of structurally related toxins which
CC share similar biological activities. They stimulate CD4+ and
CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
CC elements on the lateral face of the T-cell receptor (TCR) while
CC simultaneously binding the lateral face of the class II major
CC histocompatibility complex (MHC) of antigen presenting cells. This causes
CC aberrant proliferation of T-cells, which stimulates other components of
CC the immune system, causing injury to the host. The peptides are used to
CC prevent, treat or protect against toxic shock and septic shock resulting
CC from bacterial infections in mammals, particularly humans. The peptides
CC are used for inducing serum antibodies that bind at least one
CC staphylococcal enterotoxin or streptococcal exotoxin and both the
CC peptides and antibodies can be used in diagnostic assays to aid in the
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
CC acids encoding a peptide of the invention can be used for the production
CC of the peptides for diagnostic reagents, as vaccines and for therapies
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
CC of the peptides can be used in immunotherapy and immunoprophylaxis when
CC expressed in humans. The antibodies are used for passive immunisation or
CC therapy to prevent or increase resistance to toxic shock syndrome or
CC septic shock and to ameliorate the effects of conditions associated with
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The
CC amino acid sequences of the peptides are sufficiently common that they
CC can be used for eliciting antibodies which are cross-reactive with toxins
CC derived from various bacteria. Sequences AAV97838-Y978343 represent the
CC synthetic peptides based on consensus consensus regions 1 and 2 of
CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins
CC These peptides can be administered to a mammal to raise serum antibodies
CC for protection against or amelioration of toxic or septic shock.
XX
SQ Sequence 12 AA:
Query Match 90.1%; Score 64; DB 21; Length 12;
Best Local Similarity 91.7%; Pred. No. 7.1e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CMYGVTLHEGN 12
Db 1 CMYGVTEHEGN 12
IIIIIIIIII
RESULT 3
AAV97846
ID AAV97846 standard; peptide: 12 AA.
XX
AC AAV97846;
XX
DT 29-AUG-2000 (first entry)
XX
DE Staphylococcus aureus enterotoxin SEC, conserved region 1.
XX
KM Staphylococcal infection; enterotoxin; septic shock; toxic shock;
KW vaccine; antibody.

OS Staphylococcus aureus.
XX WO200020598-A1.
XX 13-APR-2000.
XX 24-SEP-1999; 99WO-US22180.
XX 07-OCT-1998; 98US-0168303.
XX 18-JUN-1999; 99US-0335581.
XX (UYRO) UNIV ROCKEFELLER.
XX Bannan JD, Visvanathan K, Zabriskie JB:
XX WPI: 2000-303782/26.
XX
XX Peptides useful for preventing and reducing the symptoms of toxic shock
XX syndrome and septic shock from staphylococcal and streptococcal
XX infections -
XX
XX Example 1; Page 72; 115pp; English.
XX
XX The invention relates to novel peptides (AA97838-Y97843) comprising a
XX consensus amino acid sequence derived from two conserved regions
XX (regions 1 and 2) of Staphylococcus aureus enterotoxins and
XX streptococcal pyrogenic toxins. Consensus region 1a (a preferred
XX consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N
XX (AA97863) and consensus region 2a (a preferred consensus region 2) has
XX the sequence K-X6-X7-X8-
XX X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
XX (AA97864), where: X1, X8, X13 and X24 are each independently selected
XX from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
XX X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
XX the group consisting of any amino acid;
XX X3, X5 and X26 are each independently selected from the group consisting
XX of any amino acid and of no amino acid;
XX X27 is either L or Y.
XX
XX The invention also relates to serum antibodies induced by the peptides
XX which provide protection against, or reduce the severity of toxic shock
XX and septic shock caused by the staphylococcal and streptococcal
XX pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
XX the enterotoxins of Staphylococcus aureus (which are also pyrogenic
XX exotoxins) constitute a family of structurally related toxins which
XX share similar biological activities. They stimulate CD4+ and
XX gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
XX elements on the lateral face of the T-cell receptor (TCR) while
XX simultaneously binding the lateral face of the class II major
XX histocompatibility complex (MHC) of antigen presenting cells. This causes
XX aberrant proliferation of T-cells, which stimulates other components of
XX the immune system, causing injury to the host. The peptides are used to
XX prevent, treat or protect against toxic shock and septic shock resulting
XX from bacterial infections in mammals, particularly humans. The peptides
XX are used for inducing serum antibodies that bind at least one
XX staphylococcal enterotoxin or streptococcal exotoxin and both the
XX peptides and antibodies can be used in diagnostic assays to aid in the
XX diagnosis of disease related to the presence of bacterial toxins. Nucleic
XX acids encoding a peptide of the invention can be used for the production
XX of the peptides for diagnostic reagents, as vaccines and for therapies
XX for pyrogenic exotoxin related diseases. Vectors expressing high levels
XX of the peptides can be used in immunotherapy and immunoprophylaxis when
XX expressed in humans. The antibodies are used for passive immunisation or
XX therapy to prevent or increase resistance to toxic shock syndrome or
XX septic shock and to ameliorate the effects of conditions associated with
XX the presence of staphylococcal or streptococcal pyrogenic toxins. The
XX amino acid sequences of the peptides which are cross-reactive with toxins
XX derived from various bacteria. Sequences AA97844-Y97852 represent
XX conserved region 1 of various Staphylococcus aureus enterotoxins and
XX Group A streptococcal pyrogenic exotoxins.
XX
XX Sequence 12 AA:

Query Match 90.1%; Score 64; DB 21; Length 12;
Best Local Similarity 83.3%; Pred. No. 7,1e-05;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 CMYGGVTLHEGN 12
Db 1 cmgygltkhegn 12

RESULT 4

AA972176
ID AA972176 standard; peptide; 12 AA.

AC AA972176;

DT 24-APR-2001 (first entry)

DE Peptide #6343, derived from streptococcal and staphylococcal toxins.

XX Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;

KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;

KM streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.

OS Streptococcus sp.

XX Staphylococcus sp.

XX WO200078790-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000MO-US16680.

XX 18-JUN-1999; 99US-0336627.

XX (UYRO) UNIV ROCKEFELLER.

XX Visvanathan K, Zabriskie JB;

XX WPI: 2001-080820/09.

XX Providing protection against, and reducing the severity of, human

PT immunodeficiency virus infections and associated deleterious effects,

PT using peptides from homologous sequences of staphylococcal and

PT streptococcal toxins -

PS Claim 5; Page 38; 76pp; English.

XX The present sequence is peptide #6343, derived from region 1 of

XX the homologous sequences of staphylococcal enterotoxin and

XX streptococcal pyrogenic exotoxin.

XX The peptide, nucleic acid encoding the peptide and antibody (Ab) produced

XX against the peptide are useful for inhibiting blastogenesis of

XX mononuclear cells (eg. T cells) in the presence of human immunodeficiency

XX virus (HIV), inhibiting HIV replication and protecting a mammal against

XX the deleterious effects of HIV. The peptide is also used to ameliorate

XX the effects of autoimmune diseases associated with the presence of HIV.
XX The Ab is used for passively immunising a mammal against the deleterious
XX effects of HIV.
XX
XX Sequence 12 AA:

Query Match 90.1%; Score 64; DB 22; Length 12;

Best Local Similarity 91.7%; Pred. No. 7,1e-05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
Db 1 cmgygvttehegn 12

```

RESULT 5
AAV72184
ID AAV72184 standard; peptide: 12 AA.
XX
AC AAV72184;
XX
DT 24-APR-2001 (first entry)
XX
DE Peptide from region 1 of staphylococcal enterotoxin SEC.
XX
KW Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;
XX autoimmune disease; immunisation.
XX
OS Staphylococcus sp.
XX
PN WO200078790-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16680.
XX
PR 18-JUN-1999; 99US-0336627.
XX
PA (UVRQ ) UNIV ROCKEFELLER.
XX
PI Visvanathan K, Zabriskie JB;
XX
DR WPI; 2001-080820/09.
XX
PT Providing protection against, and reducing the severity of, human
PT immunodeficiency virus infections and associated deleterious effects,
PT using peptides from homologous sequences of staphylococcal and
PT streptococcal toxins
XX
PS Disclosure; Page 36; 76pp; English.
XX
XX The present sequence is a peptide from region 1 of staphylococcal
XX enterotoxin SEC.
XX The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
XX against the peptide are useful for inhibiting blastogenesis of
XX mononuclear cells (eg. T cells) in the presence of human immunodeficiency
XX virus (HIV), inhibiting HIV replication and protecting a mammal against
XX the deleterious effects of HIV. The peptide is also used to ameliorate
XX the effects of autoimmune diseases associated with the presence of HIV.
XX The Ab is used for passively immunising a mammal against the deleterious
XX effects of HIV.
XX
SQ Sequence 12 AA;

```

Query Match 90.1%; Score 64; DB 22; Length 12;
 Best Local Similarity 83.3%; Pred. No. 7.1e-05;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CMYGGVTLHEGN 12
DB 1 cmysgltkhegn 12

```

RESULT 6
 AAV72424
 ID AAV72424 standard; peptide: 14 AA.
 XX
 AC AAV72424;
 XX
 DT 22-DEC-1998 (first entry)
 XX
 DE Peptide #3 for reducing symptoms of toxic shock syndrome.
 XX
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.

```

XX
OS Synthetic.
OS Staphylococcus sp.
OS Streptococcus sp.
XX
PN WO9845325-A1.
XX
PD 15-OCT-1998.
XX
PF 01-APR-1998; 98WO-US06663.
XX
PR 07-APR-1997; 97US-0838413.
XX
PA (UVRQ ) UNIV ROCKEFELLER.
XX
PI Bannan JD, Zabriskie JB;
XX
DR WPI; 1998-568335/48.
XX
PT New peptides that generate antibodies against staphylococcal and
PT streptococcal toxins - used to diagnose, treat or prevent toxic
PT shock and autoimmune diseases
XX
PS Claim 4; Page 53; 69pp; English.
XX
XX The present invention describes peptides having consensus sequences #1
XX or #2, optionally as part of a larger molecule of size at least 6-8 kD.
XX Where consensus sequence #1 and #2 are: X25X26YGGX1RX23X4X5N #1,
XX KX6X78X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X3X24Y #2, where
XX X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
XX or are absent; X27 = L or Y; all other X may be any aa. The peptides
XX can be used to generate serum antibodies (Ab) that bind at least one
XX staphylococcal enterotoxin (SE) or streptococcal endotoxin (SE). Ab
XX are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
XX usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
XX cells in presence of these toxins (i.e. to protect against or alleviate
XX toxic shock or autoimmune disease associated with bacterial infections);
XX and (iii) for passive immunisation against effects of the toxins. The
XX peptides generate Ab that are cross-reactive with toxins from a variety
XX of bacteria. The present sequence represents a specifically claimed
XX example of a peptide of the present invention.
XX
SQ Sequence 14 AA;

```

Query Match 90.1%; Score 64; DB 19; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.4e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CMYGGVTLHEGN 12
DB 1 cmysgvtkehegn 12

```

RESULT 7
 AAV97840
 ID AAV97840 standard; peptide: 14 AA.
 XX
 AC AAV97840;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6344.
 XX
 KW Pyrogenic exotoxin; enterotoxin; streptococcal infection;
 KW staphylococcal infection; septic shock; toxic shock; vaccine;
 KW antibody.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS Streptococcus sp. 'Group A'.
 XX
 PN WO200020598-A1.

XX 13-APR-2000.
 PD
 PF 24-SEP-1999; 99MO-US22180.
 XX
 PR 07-OCT-1998; 9805-0168303.
 PR 18-JUN-1999; 99US-0335581.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 PI Bannan JD, Visvanathan K, Zabriskie JB;
 DR WPI: 2000-303782/26.
 XX
 PT Peptides useful for preventing and reducing the symptoms of toxic shock
 PT syndrome and septic shock from staphylococcal and streptococcal
 PT infections -
 XX
 PS Claim 4; Page 88; 115pp; English.
 XX
 CC The invention relates to novel peptides (AAV97838-Y97843) comprising a
 CC consensus amino acid sequence derived from two conserved regions
 CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
 CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
 CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N
 CC (AAV97863) and consensus region 2a (a preferred consensus region 2) has
 CC the sequence K-X6-X7-X8-
 CC X3-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
 CC (AAV97864), where: X1, X8, X13 and X24 are each independently selected
 CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
 CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
 CC the group consisting of any amino acid:
 CC X3, X5 and X26 are each independently selected from the group consisting
 CC of any amino acid and of no amino acid;
 CC X27 is either L or Y.
 CC The invention also relates to serum antibodies induced by the peptides
 CC which provide protection against, or reduce the severity of toxic shock
 CC and septic shock caused by the staphylococcal and streptococcal
 CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococcal and
 CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic
 CC exotoxins) constitute a family of structurally related toxins which
 CC share similar biological activities. They stimulate CD4+, CD8+ and
 CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
 CC elements on the lateral face of the T-cell receptor (TCR) while
 CC simultaneously binding the lateral face of the class II major
 CC histocompatibility complex (MHC) of antigen presenting cells. This causes
 CC aberrant proliferation of T-cells, which stimulates other components of
 CC the immune system, causing injury to the host. The peptides are used to
 CC prevent, treat or protect against toxic shock and septic shock resulting
 CC from bacterial infections in mammals, particularly humans. The peptides
 CC are used for inducing serum antibodies that bind at least one
 CC staphylococcal enterotoxin or streptococcal exotoxin and both the
 CC peptides and antibodies can be used in diagnostic assays to aid in the
 CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
 CC acids encoding a peptide related to the invention can be used for the production
 CC of the peptides for diagnostic reagents, as vaccines and for therapies
 CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
 CC of the peptides can be used in immunotherapy and immunoprophylaxis when
 CC expressed in humans. The antibodies are used for passive immunisation
 CC therapy to prevent or increase resistance to toxic shock syndrome or
 CC septic shock and to ameliorate the effects of conditions associated with
 CC the presence of staphylococcal or streptococcal pyrogenic toxins. The
 CC amino acid sequences of the peptides are sufficiently common that they
 CC can be used for eliciting antibodies which are cross-reactive with toxins
 CC derived from various bacteria. Sequences AAV97838-Y97833 represent the
 CC synthetic peptides based on consensus consensus regions 1 and 2 of
 CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.
 CC These peptides can be administered to a mammal to raise serum antibodies
 CC for protection against or amelioration of toxic or septic shock.
 CC
 CC Sequence 14 AA:
 CC
 CC SQ

Query Match 90.1%; Score 64; DB 21; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.4e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
 |||||
 Db 1 cmgyvtehegn 12

RESULT 8

AAV72178
 ID AAV72178 standard; peptide; 14 AA.
 XX

AC AAV72178;
 XX

DT 24-APR-2001 (first entry)
 XX

DE Peptide #6344, derived from streptococcal and staphylococcal toxins.
 XX

KW Mononuclear cell; blastogenesis; inhibitor; HIV; replication; therapy;
 KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;
 KW streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.
 XX

OS Streptococcus sp.
 OS Staphylococcus sp.
 XX

PN W0200078790-A2.
 XX

XX 28-DEC-2000.
 PD

XX 16-JUN-2000; 2000WO-US16680.
 PF

PR 18-JUN-1999; 99US-0336627.
 PR

XX (UYRQ) UNIV ROCKEFELLER.
 XX

PI Visvanathan K, Zabriskie JB;
 XX

DR WPI: 2001-080820/09.
 XX

XX providing protection against, and reducing the severity of, human
 PT immunodeficiency virus infections and associated deleterious effects,
 PT using peptides from homologous sequences of staphylococcal and
 PT streptococcal toxins -
 XX

XX Claim 5; Page 38; 76pp; English.
 PS

XX The present sequence is peptide #6344, a cross-linked polymer derived
 CC from the homologous sequences of staphylococcal enterotoxin and
 CC streptococcal pyrogenic exotoxin.
 CC The peptide, nucleic acid encoding the peptide and antibody (Ab) produced
 CC against the peptide are useful for inhibiting blastogenesis of
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against
 CC the deleterious effects of HIV. The peptide is also used to ameliorate
 CC the effects of autoimmune diseases associated with the presence of HIV.
 CC The Ab is used for passively immunising a mammal against the deleterious
 CC effects of HIV.
 CC
 CC Sequence 14 AA:
 CC
 CC SQ

Query Match 90.1%; Score 64; DB 22; Length 14;
 Best Local Similarity 91.7%; Pred. No. 8.4e-05;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
 |||||
 Db 1 cmgyvtehegn 12

RESULT 9

AAV72426

ID AAW72426 standard; peptide; 36 AA.
 XX
 AC AAW72426;
 XX
 DT 22-DEC-1998 (first entry)
 XX
 DE Peptide #5 for reducing symptoms of toxic shock syndrome.
 XX
 KW Toxic shock syndrome; immunogenic response; bacterial infection;
 KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;
 KW autoimmune disease.
 XX
 OS Synthetic.
 OS Staphylococcus sp.
 OS Streptococcus sp.
 XX
 PN W09845325-A1.
 PD 15-OCT-1998.
 XX
 PF 01-APR-1998; 98WO-US06663.
 XX
 PR 07-APR-1997; 97US-0838413.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Bannan JD, Zabriskie JB;
 XX
 DR WPI; 1998-56835/48.
 XX
 PT New peptides that generate antibodies against staphylococcal and
 PT streptococcal toxins - used to diagnose, treat or prevent toxic
 PT shock and autoimmune diseases
 XX
 PS Claim 4; Page 54; 69pp; English.
 XX
 CC The present invention describes peptides having consensus sequences #1
 CC or #2, optionally as part of a larger molecule of size at least 6-8 kD.
 CC Where consensus sequence #1 and #2 are: X25X26YG6X1X2X3X4X5N #1,
 CC K6X178X9X10X11X12X13X14X15X16R17X18X27X19X20X21X22X23X24Y #2, where
 CC X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)
 CC or are absent; X27 = L or Y; all other X may be any aa. The peptides
 CC can be used to generate serum antibodies (Ab) that bind at least one
 CC staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab
 CC are used: (i) for diagnostic detection of SPEA or SEA, SEB and SED, in
 CC usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear
 CC cells in presence of these toxins (i.e. to protect against or alleviate
 CC toxic shock or autoimmune disease associated with bacterial infections);
 CC and (iii) for passive immunisation against effects of the toxins. The
 CC peptides generate Ab that are cross-reactive with toxins from a variety
 CC of bacteria. The present sequence represents a specifically claimed
 CC example of a peptide of the present invention.
 XX
 SQ Sequence 36 AA;
 XX
 QY 1 CMYGVTLHGN 12
 DB 1 CMYGVTLHGN 12
 DB 1 CMYGVTLHGN 12
 XX
 RESULT 10
 AAY97842
 ID AAY97842 standard; peptide; 36 AA.
 XX
 AC AAY97842;
 XX
 DT 29-AUG-2000 (first entry)
 XX

DE Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6347.
 XX
 KW Pyrogenic exotoxin; enterotoxin; streptococcal infection;
 KW staphylococcal infection; septic shock; toxic shock; vaccine;
 KW antibody.
 XX
 OS Synthetic.
 OS Staphylococcus aureus.
 OS Streptococcus sp. 'Group A'.
 XX
 PN W0200020598-A1.
 PD 13-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US22180.
 XX
 PR 07-OCT-1998; 98US-0168303.
 PR 18-JUN-1999; 99US-0335581.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Bannan JD, Visvanathan K, Zabriskie JB;
 XX
 DR WPI; 2000-303782/26.
 XX
 PT Peptides useful for preventing and reducing the symptoms of toxic shock
 PT syndrome and septic shock from staphylococcal and streptococcal
 PT infections -
 XX
 PS Claim 4; Page 88; 115pp; English.
 XX
 CC The invention relates to novel peptides (AAY97838-Y97843) comprising a
 CC consensus amino acid sequence derived from two conserved regions
 CC (regions 1 and 2) of Staphylococcus aureus enterotoxins and
 CC streptococcal pyrogenic toxins. Consensus region 1a (a preferred
 CC consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N
 CC (AAY97863) and consensus region 2a (a preferred consensus region 2) has
 CC the sequence K-X6-X7-X8-
 CC X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
 CC (AAY97864), where: X1, X8, X13 and X24 are each independently selected
 CC from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
 CC X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
 CC the group consisting of any amino acid;
 CC X3, X5 and X26 are each independently selected from the group consisting
 CC of any amino acid and of no amino acid;
 CC X27 is either L or Y.
 CC The invention also relates to serum antibodies induced by the peptides
 CC which provide protection against, or reduce the severity of toxic shock
 CC and septic shock caused by the staphylococcal and streptococcal
 CC pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
 CC the enterotoxins of Staphylococcus aureus (which are also pyrogenic
 CC exotoxins) constitute a family of structurally related toxins which
 CC share similar biological activities. They stimulate CD4+ and CD8+ and
 CC gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
 CC elements on the lateral face of the T-cell receptor (TCR) while
 CC simultaneously binding the lateral face of the class II major
 CC histocompatibility complex (MHC) of antigen presenting cells. This causes
 CC aberrant proliferation of T-cells, which stimulates other components of
 CC the immune system, causing injury to the host. The peptides are used to
 CC prevent, treat or protect against toxic shock and septic shock resulting
 CC from bacterial infections in mammals, particularly humans. The peptides
 CC are used for inducing serum antibodies that bind at least one
 CC staphylococcal enterotoxin or streptococcal exotoxin and both the
 CC peptides and antibodies can be used in diagnostic assays to aid in the
 CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
 CC acids encoding a peptide of the invention can be used for the production
 CC of the peptides for diagnostic reagents, as vaccines and for therapies
 CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
 CC of the peptides can be used in immunotherapy and immunoprophylaxis when
 CC expressed in humans. The antibodies are used for passive immunisation
 CC therapy to prevent or increase resistance to toxic shock syndrome or
 CC septic shock and to ameliorate the effects of conditions associated with
 CC the presence of staphylococcal or streptococcal pyrogenic toxins. The

CC amino acid sequences of the peptides are sufficiently common that they
CC can be used for eliciting antibodies which are cross-reactive with toxins
CC derived from various bacteria. Sequences AAY97838-Y97843 represent the
CC synthetic peptides based on consensus consensus regions 1 and 2 of
CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.
CC These peptides can be administered to a mammal to raise serum antibodies
CC for protection against or amelioration of toxic or septic shock.

SO Sequence 36 AA:

Query Match 90.1%; Score 64; DB 21; Length 36;
Best Local Similarity 91.7%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
|||||
Db 1 cmgygvtehgn 12

RESULT 11

AAY72180
ID AAY72180 standard; peptide; 36 AA.

AC AAY72180;

DT 24-APR-2001 (first entry)

PEptide #6347, derived from streptococcal and staphylococcal toxins.

Mononuclear cell; blastogenesis; inhibitor: HIV; replication; therapy;

KW staphylococcal enterotoxin; human immunodeficiency virus; T cell;

KW streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.

OS Streptococcus sp.

OS Staphylococcus sp.

PN MO200078790-A2.

PD 28-DEC-2000.

PF 16-JUN-2000; 2000MO-US16680.

PR 18-JUN-1999; 99US-0336627.

PA (UYRQ) UNIV ROCKEFELLER.

PI Visvanathan K, Zabriskie JB;

DR WPI; 2001-080820/09.

PT Providing protection against, and reducing the severity of, human

PT immunodeficiency virus infections and associated deleterious effects,

PT using peptides from homologous sequences of staphylococcal and

PT streptococcal toxins

PS Claim 5; Page 38; 76pp: English.

XX The present sequence is peptide #6347, derived from the homologous

XX sequences of staphylococcal enterotoxin and streptococcal pyrogenic

XX exotoxin.

XX The peptide, nucleic acid encoding the peptide and antibody (Ab) produced

XX against the peptide are useful for inhibiting blastogenesis of

XX mononuclear cells (eg. T cells) in the presence of human immunodeficiency

XX virus (HIV), inhibiting HIV replication and protecting a mammal against

XX the deleterious effects of HIV. The peptide is also used to ameliorate

XX the effects of autoimmune diseases associated with the presence of HIV.

XX The Ab is used for passively immunising a mammal against the deleterious

XX effects of HIV.

XX Sequence 36 AA:

Query Match 90.1%; Score 64; DB 22; Length 36;
Best Local Similarity 91.7%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
|||||
Db 1 cmgygvtehgn 12

RESULT 12

AAW72427
ID AAW72427 standard; peptide; 38 AA.

AC AAW72427;

DT 22-DEC-1998 (first entry)

DE Peptide #6 for reducing symptoms of toxic shock syndrome.

DE Toxic shock syndrome; immunogenic response; bacterial infection;

KW staphylococcal enterotoxin; streptococcal pyrogenic toxin; antibody;

KW autoimmune disease.

OS Synthetic.

OS Staphylococcus sp.

OS Streptococcus sp.

PN MO9845325-A1.

PD 15-OCT-1998.

PF 01-APR-1998; 98MO-US06663.

PR 07-APR-1997; 97US-0838413.

PA (UYRQ) UNIV ROCKEFELLER.

PI Bannan JD, Zabriskie JB;

DR WPI; 1998-568335/48.

PT New peptides that generate antibodies against staphylococcal and

PT streptococcal toxins - used to diagnose, treat or prevent toxic

PT shock and autoimmune diseases

PS Claim 4; Page 54; 69pp: English.

XX The present invention describes peptides having consensus sequences #1

XX or #2, optionally as part of a larger molecule of size at least 6-8 kD.

XX Where consensus sequence #1 and #2 are: X25X26YGGX19X23X4X5N #1,

XX KX6X7X8X9X10X11X12X13DX14X15X16RX17X18X27X19X20X21X22X23X24Y #2, where

XX X1, X8, X13 and X24 = L, I or V; X3, X25 and X26 = any amino acid (aa)

XX CC or are absent; X27 = L or Y; all other X may be any aa. The peptides

XX can be used to generate serum antibodies (Ab) that bind at least one

XX staphylococcal enterotoxin (SE) or streptococcal endotoxin (SPE). Ab

XX are used: (i) for diagnostic detection of SPEA or SPE, SEB and SED, in

XX usual immunoassays; (ii) to inhibit blastogenesis of human mononuclear

XX cells in presence of these toxins (i.e. to protect against or alleviate

XX toxic shock or autoimmune disease associated with bacterial infections);

XX CC and (iii) for passive immunisation against effects of the toxins. The

XX peptides generate Ab that are cross-reactive with toxins from a variety

XX of bacteria. The present sequence represents a specifically claimed

XX example of a peptide of the present invention.

XX Sequence 38 AA:

Query Match 90.1%; Score 64; DB 19; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
|||||
Db 1 cmgygvtehgn 12

Db 1 cmvgvtehegn 12

RESULT 13
AAV97843
ID AAV97843 standard; peptide: 38 AA.

AC AAV97843;
DE 29-AUG-2000 (first entry)

XX Staphylococcal/streptococcal pyrogenic toxin-derived peptide, 6348.
XX
XX Pyrogenic exotoxin; enterotoxin; streptococcal infection;
XX staphylococcal infection; septic shock; toxic shock; vaccine;
XX antibody.
XX
XX Synthetic.
XX Staphylococcus aureus.
XX Streptococcus sp. Group A.
XX
XX WO200020598-A1.
XX
XX 13-APR-2000.
XX
XX 24-SEP-1999; 99WO-US22180.
XX
XX 07-OCT-1998; 98US-0168303.
XX 18-JUN-1999; 99US-0335581.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Bannan JD, Visvanathan K, Zabriskie JB;
XX
XX WPI: 2000-303782/26.
XX
XX Peptides useful for preventing and reducing the symptoms of toxic shock
XX syndrome and septic shock from staphylococcal and streptococcal
XX infections .
XX
XX Claim 4; Page 88; 115pp; English.

The invention relates to novel peptides (AAV97838-Y97843) comprising a
consensus amino acid sequence derived from two conserved regions
(regions 1 and 2) of Staphylococcus aureus enterotoxins and
streptococcal pyrogenic toxins. Consensus region 1a (a preferred
consensus region 1) has the sequence X25-X26-Y-G-G-X1-T-X2-X3-X4-X5-N
(AAV97863) and consensus region 2a (a preferred consensus region 2) has
the sequence K-X6-X7-X8-
X9-X10-X11-X12-X13-D-X14-X15-X16-R-X17-X18-X27-X19-X20-X21-X22-X23-X24-Y
(AAV97864), where: X1, X8, X13 and X24 are each independently selected
from L, I and V; X2, X4, X5, X6, X7, X9, X10, X11, X12, X14, X15, X16,
X17, X18, X19, X20, X21, X22 and X23 are each independently selected from
the group consisting of any amino acid;
X3, X5 and X26 are each independently selected from the group consisting
of any amino acid and of no amino acid;
X27 is either L or Y.
The invention also relates to serum antibodies induced by the peptides
which provide protection against, or reduce the severity of toxic shock
and septic shock caused by the staphylococcal and streptococcal
pyrogenic toxins. The pyrogenic exotoxins of Group A streptococci and
the enterotoxins of Staphylococcus aureus (which are also pyrogenic
exotoxins) constitute a family of structurally related toxins which
share similar biological activities. They stimulate CD4+, CD8+ and
gamma-delta+ T-cells by binding the beta-chain variable region (V-beta)
elements on the lateral face of the T-cell receptor (TCR) while
simultaneously binding the lateral face of the class II major
histocompatibility complex (MHC) of antigen presenting cells. This causes
aberrant proliferation of T-cells, which stimulates other components of
the immune system, causing injury to the host. The peptides are used to
prevent, treat or protect against toxic shock and septic shock resulting
from bacterial infections in mammals, particularly humans. The peptides
are used for inducing serum antibodies that bind at least one

CC staphylococcal enterotoxin or streptococcal exotoxin and both the
CC peptides and antibodies can be used in diagnostic assays to aid in the
CC diagnosis of disease related to the presence of bacterial toxins. Nucleic
CC acids encoding a peptide of the invention can be used for the production
CC of the peptides for diagnostic reagents, as vaccines and for therapies
CC for pyrogenic exotoxin related diseases. Vectors expressing high levels
CC of the peptides can be used in immunotherapy and immunoprophylaxis when
CC expressed in humans. The antibodies are used for passive immunisation
CC therapy to prevent or increase resistance to toxic shock syndrome or
CC septic shock and to ameliorate the effects of conditions associated with
CC the presence of staphylococcal or streptococcal pyrogenic toxins. The
CC amino acid sequences of the peptides are sufficiently common that they
CC can be used for eliciting antibodies which are cross-reactive with toxins
CC derived from various bacteria. Sequences AAV97838-Y97843 represent the
CC synthetic peptides based on consensus consensus regions 1 and 2 of
CC Staphylococcus aureus and Group A streptococcal pyrogenic toxins.
CC These peptides can be administered to a mammal to raise serum antibodies
CC for protection against or amelioration of toxic or septic shock.
XX
XX Sequence 38 AA;
XX
XX

Query Match 90.1%; Score 64; DB 21; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMVGVTLEHGN 12
||| ||| ||| |||
Db 1 cmvgvtehegn 12

RESULT 14
AAV72181
ID AAV72181 standard; peptide: 38 AA.
XX
XX AAV72181;
XX
XX 24-APR-2001 (first entry)
XX
XX Peptide #6348, derived from streptococcal and staphylococcal toxins.
XX
XX Mononuclear cell; blastogenesis; inhibitor; HIV replication; therapy;
XX streptococcal enterotoxin; human immunodeficiency virus; T cell;
XX streptococcal pyrogenic exotoxin; autoimmune disease; immunisation.
XX
XX Streptococcus sp.
XX
XX Staphylococcus sp.
XX
XX WO200078790-A2.
XX
XX 28-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-US16680.
XX
XX 18-JUN-1999; 99US-0336627.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Visvanathan K, Zabriskie JB;
XX
XX WPI: 2001-080820/09.
XX
XX Providing protection against, and reducing the severity of, human
XX immunodeficiency virus infections and associated deleterious effects,
XX using peptides from homologous sequences of staphylococcal and
XX streptococcal toxins .
XX
XX Claim 5; Page 38; 76pp; English.

The present sequence is peptide #6348, a cross-linked polymer derived
from the homologous sequences of staphylococcal enterotoxin and
streptococcal pyrogenic exotoxin.
The peptide, nucleic acid encoding the peptide and antibody (Ab) produced

CC Against the peptide are useful for inhibiting blastogenesis of
 CC mononuclear cells (eg. T cells) in the presence of human immunodeficiency
 CC virus (HIV), inhibiting HIV replication and protecting a mammal against
 CC the deleterious effects of HIV. The peptide is also used to ameliorate
 CC the effects of autoimmune diseases associated with the presence of HIV.
 CC The Ab is used for passively immunising a mammal against the deleterious
 CC effects of HIV.
 XX

Sequence 38 AA:

Query Match 90.1%; Score 64; DB 22; Length 38;
 Best Local Similarity 91.7%; Pred. NO. 0.00025;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
 ||||| ||||
 Db 1 cmYggvtehegn 12

RESULT 15

AAR13208
 ID AAR13208 standard; Protein; 238 AA.

AC AAR13208;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin C3.

KW SEC3; cancer treatment; pyrogen; tumouricide.

OS Staphylococcus aureus.

XX WO9110680-A.

XX 25-JUL-1991.

XX 17-JAN-1991; 91WO-US00342.

XX 17-JAN-1990; 90US-046577.

PA (TERM/) TERMAN D S.

XX Terman DS;

DR WPI: 1991-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 XX
 XX Disclosure: Fig 1; 74pp; English.

CC SEC3 was isolated and purified from S.aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEC3. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydrophobic profiles.
 CC See AAR13203-R13211.

XX Sequence 238 AA:

Query Match 90.1%; Score 64; DB 12; Length 238;
 Best Local Similarity 83.3%; Pred. NO. 0.0019;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12

Db 109 cmYggvtehegn 120
 |||||:| ||||

Search completed: January 2, 2002, 20:48:13
 Job time: 10129 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2002, 20:49:24 ; Search time 56.72 Seconds
(without alignments)
16.116 Million cell updates/sec

Title: US-09-335-581A-34
Perfect score: 71
Sequence: 1 CMYGGVTLHEGN 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	90.1	266	1 ENSAC1	enterotoxin C-1 pr
2	64	90.1	266	2 A60114	enterotoxin C-2 pr
3	64	90.1	266	3 S11885	enterotoxin C3 - S
4	62	87.3	257	2 A28664	enterotoxin A prec
5	62	87.3	257	2 A28179	enterotoxin B prec
6	61	85.9	250	1 A26152	streptococcal pyro
7	60	84.5	236	2 S18789	exotoxin A precurs
8	60	84.5	236	2 S18786	exotoxin type A pr
9	60	84.5	236	2 S18783	exotoxin type A pr
10	60	84.5	251	1 S29659	exotoxin type A pr
11	59	83.1	266	1 ENSAB6	enterotoxin B prec
12	58	81.7	258	2 A33953	enterotoxin D prec
13	43	60.6	841	2 J00647	preprotein translo
14	42	59.2	270	2 B48826	high chorolytic h
15	42	59.2	279	2 C48826	high chorolytic h
16	42	59.2	895	2 T11979	preprotein translo
17	41.5	58.5	463	2 A38463	fibrinogen beta ch
18	41	57.7	185	2 S04792	mobilization prote
19	41	57.7	437	2 S69881	phosphorylase hy
20	41	57.7	437	2 S67305	phosphorylase hy
21	40	56.3	810	2 T10736	Net-homolog protei
22	40	56.3	968	2 A37867	transcription fact
23	39	54.9	156	2 A35697	transposase (09) B
24	39	54.9	156	2 B83855	transposase (09) B
25	39	54.9	156	2 G83886	transposase (09) B
26	39	54.9	156	2 B84005	transposase (09) B
27	39	54.9	156	2 A84054	transposase (09) B
28	39	54.9	156	2 B84083	transposase (09) B
29	39	54.9	156	2 F84084	transposase (09) B

30	39	54.9	156	2 H83671	transposase (09) B
31	39	54.9	156	2 E83683	transposase (09) B
32	39	54.9	198	2 S54733	ribosomal protein
33	39	54.9	767	2 A35645	major surface prot
34	39	54.9	805	2 T40739	rmf3-pil1 helicase
35	39	54.9	805	2 T47241	RMH3/Pil1 helicase
36	39	54.9	916	2 D83093	secretion protein
37	38	53.5	265	2 S38380	Hroxl protein - Ca
38	38	53.5	347	2 T26349	hypothetical prote
39	38	53.5	347	2 T35013	probable membrane
40	38	53.5	813	2 T40622	translation elonga
41	38	53.5	871	2 C72238	preprotein translo
42	38	53.5	1028	2 E85089	probable transposo
43	37	52.1	159	2 T30926	hypothetical prote
44	37	52.1	284	2 H84124	3-hydroxybutyryl-C
45	37	52.1	295	2 C83244	conserved hypothet

ALIGNMENTS

```
RESULT 1
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
A:Accession: S06356; A01816
R:Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness
A:Reference number: S06356; MUID:88038352
A:Accession: S06356
A:Molecule type: DNA
A:Residues: 1266 <BOH>
A:Cross-references: EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567
R:Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A:Reference number: A01816; MUID:83213327
A:Accession: A01816
A:Molecule type: Protein
A:Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C:Gene: entC1
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-1 #status experimental <MAT>
F:120-137/Disulfide bonds: #status experimental

Query Match          90.1%  Score 64: DB 1: Length 266:
Best Local Similarity 83.3%: Pred. No. 0.00091:
Matches 10: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

OY 1 CMYGGVTLHEGN 12
DB 137 CMYGGVTLHEGN 148

RESULT 2
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphylococcal enterotox
A:Reference number: A60114; MUID:89277549
A:Accession: A60114
A:Status: not compared with conceptual translation
```

A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Accession: B60114
A:Molecule type: protein
A:Residues: 28-66 <BOH2>
R:Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
A:Reference number: A33866; MUID:89327174
A:Accession: A33866
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <COU>
A:Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
C:Genetics:
A:Gene: entC2
C:Superfamily: enterotoxin B
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 90.1%; Score 64; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. NO. 0.00091;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
|||||:|||||
DB 137 CMYGVTLHEGN 148

RESULT 3
S11885
enterotoxin C3 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C:Accession: S11885
R:Howe, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compar
A:Reference number: S11885; MUID:90220508
A:Accession: S11885
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <HOV>
A:Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C:Superfamily: enterotoxin B

Query Match 90.1%; Score 64; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. NO. 0.00091;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
|||||:|||||
DB 137 CMYGVTLHEGN 148

RESULT 4
A28664
enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28664; A29566
R:Betley, M.J.; Mekalanos, J.J.
J. Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; MUID:8806892
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-references: GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121
A:Experimental source: strain FR1337
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.

J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; MUID:87222293
A:Accession: A29566
A:Molecule type: protein
A:Residues: 25-241, 'S', 243-257 <HUA>
C:Genetics:
A:Gene: entA
A:Map position: 6
C:Superfamily: enterotoxin B

Query Match 87.3%; Score 62; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. NO. 0.002;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
|||||:|||||
DB 130 CMYGVTLHDNN 141

RESULT 5
A28179
enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28179
R:Couch, J.L.; Solits, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gen
A:Reference number: A28179; MUID:86257005
A:Accession: A28179
A:Molecule type: DNA
A:Residues: 1-257 <COU>
A:Cross-references: GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002
C:Superfamily: enterotoxin B

Query Match 87.3%; Score 62; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. NO. 0.002;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
|||||:|||||
DB 130 CMYGVTLHDNN 141

RESULT 6
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26152
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to
A:Reference number: A26152; MUID:86284313
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
A:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 85.9%; Score 61; DB 1; Length 250;
Best Local Similarity 83.3%; Pred. NO. 0.0029; 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
|||||:|||||
DB 128 CMYGVTLHEGN 139

```
RESULT 7
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61573; NID:q47303; PIDN:CAA43771.1; PID:q47304
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <Sig>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 84.5%; Score 60; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 0.0041;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CMYGVTLHEGN 12
|:||||| |||
Db 120 CTVGVTHNHEGN 131

RESULT 8
S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isol
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain
Isolate United Kingdom; strain MGAS496 isolate Germany
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323
A:Accession: S18786
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61561; NID:q47297; PIDN:CAA43759.1; PID:q47298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18787
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61562; NID:q47299; PIDN:CAA43760.1; PID:q47300
A:Experimental source: strain MGAS251 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61563; NID:q47301; PIDN:CAA43761.1; PID:q47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
```

```
A:Residues: 1-236 <NEV>
A:Cross-references: EMBL:X61564; NID:q47305; PIDN:CAA43762.1; PID:q47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18792
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61565; NID:q47311; PIDN:CAA43763.1; PID:q47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18795
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEH>
A:Cross-references: EMBL:X61566; NID:q47317; PIDN:CAA43764.1; PID:q47318
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18799
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NES>
A:Cross-references: EMBL:X61567; NID:q47325; PIDN:CAA43765.1; PID:q47326
A:Experimental source: strain MGAS496 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <Sig>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 84.5%; Score 60; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 0.0041;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CMYGVTLHEGN 12
|:||||| |||
Db 120 CTVGVTHNHEGN 131

RESULT 9
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 I
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene en
A:Reference number: S18782; MUID:92044323
A:Accession: S18783
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61568; NID:q47289; PIDN:CAA43766.1; PID:q47290
A:Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18793
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61569; NID:q47313; PIDN:CAA43767.1; PID:q47314
A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61570; NID:q47315; PIDN:CAA43768.1; PID:q47316
```

A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18801
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <MEY>
A:Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334
A:Experimental source: strain MGAS624 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18798
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A:Experimental source: strain MGAS495 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: SPEA3
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 84.5%; Score 60; DB 2; Length 236;
Best local similarity 83.3%; Pred. No. 0.0041;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
Db 120 CIGGVTHNHN 131

RESULT 10
S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12

N:Alternate names: erythrogenic toxin; scarlet fever toxin
C:Species: Streptococcus pyogenes phage T12
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

R:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R:Weeks, C.R.; Farrell, J.J.
Infected Immun. 52, 144-150, 1986

A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g
A:Reference number: S29659; MOID:8616804
A:Accession: S29659
A:Molecule type: DNA
A:Residues: 1-251 <MEB>

A:Cross-references: GB:U04053; EMBL:M19350; NID:g1877426; PIDN:AA048686.1; PID:g1877430
R:Nelson, K.; Schliefert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991

A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MOID:92044323
A:Accession: S18782
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 9-244 <NEH>
A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288

A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18784
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 9-244 <NEA>
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43755.1; PID:g47292

A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18785
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 9-244 <NEZ>
A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294

A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned ph
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A:Accession: S18791
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEV>
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18796
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEO>
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320
A:Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18797
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEH>
A:Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18800
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-228 <NES>
A:Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328
A:Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: SPEA1
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 84.5%; Score 60; DB 1; Length 251;
Best local similarity 83.3%; Pred. No. 0.0043;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
Db 128 CIGGVTHNHN 139

RESULT 11

ENSAB6
enterotoxin B precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999

R:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan, S.A.

J. Bacteriol. 166, 29-33, 1986

A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MOID:86168029
A:Accession: S27360
A:Molecule type: DNA
A:Residues: 1-266 <RON>

A:Cross-references: EMBL:M1118; NID:g152999; PIDN:AAA86550.1; PID:g153000
A:Experimental source: strain S6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bro
A:Reference number: A92065; MOID:71007902
A:Accession: A92065
A:Molecule type: protein

A:Residues: 28-95, 'NND', '59-68', 'NE', '71', 'FDLIYL', '78-117', '119-127', 'N', '129', 'D', '131-132', 'EN
A:Experimental source: strain S-6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compos
A:Reference number: A92064; MOID:71007901
A:Contents: annotation; chymotryptic peptides

R: Huang, I. Y.; Bergdoll, M. S.
J. Biol. Chem. 245, 3493-3510, 1970
A: Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition
A: Reference number: A92063; MUID: 71007900
A: Contents: annotation; tryptic peptides
R: Schantz, E. J.; Roessler, W. G.; Wagnan, J.; Spero, L.; Dunmery, D. A.; Bergdoll, M. S.
Biochemistry 4, 1011-1016, 1965
A: Title: Purification of staphylococcal enterotoxin B.
A: Reference number: A90548; MUID: 66035792
A: Contents: annotation; biological source of protein
R: Alakhov, V. Y.; Klinsky, E. Y.; Kolosov, M. I.; Maurer-Fogy, I.; Moskaleva, E. Y.; Sveshnik
Eur. J. Biochem. 209, 823-828, 1992
A: Title: Identification of functionally active fragments of staphylococcal enterotoxin B
A: Reference number: S27240; MUID: 93049338
A: Accession: S27240
A: Molecule type: Protein
A: Residues: 28-42:128-148 <ALA>
C: Superfamily: enterotoxin B
C: Keywords: enterotoxin; extracellular protein; toxin
F: 1-27/Domain: signal sequence #status predicted <SIG>
F: 28-266/Product: enterotoxin B #status experimental <MAT>
F: 120-140/Disulfide bonds: #status experimental

Query Match 83.1%; Score 59; DB 1; Length 266;
Best Local Similarity 83.3%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
DB 140 CMYGVTEHNGN 151

RESULT 12
A33953
enterotoxin D precursor - Staphylococcus aureus
C: Species: Staphylococcus aureus
C: Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C: Accession: A33953
R: Bayles, K. W.; Iandolo, J. J.
J. Bacteriol. 171, 4799-4806, 1989
A: Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A: Reference number: A33953; MUID: 69359112
A: Accession: A33953
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-258 <BAV>
A: Cross-references: GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g758691
C: Superfamily: enterotoxin B

Query Match 81.7%; Score 58; DB 2; Length 258;
Best Local Similarity 83.3%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
DB 131 CTVGVTPHEGN 142

RESULT 13
J00647
preprotein translocase secA - Bacillus subtilis
N: Alternate names: Div protein; secA protein homolog
C: Species: Bacillus subtilis
C: Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 17-Nov-2000
C: Accession: J00647; S17771; F69704
R: Sadaie, Y.; Takematsu, H.; Nakamura, K.; Yamane, K.
Gene 98, 101-105, 1991
A: Title: Sequencing reveals similarity of the wild-type div+ gene of Bacillus subtilis
A: Reference number: JN0145; MUID: 91192600
A: Accession: J00647
A: Molecule type: DNA

A: Residues: 1-841 <SAD>
A: Cross-references: GB:D10279; DDBJ:D90218; NID:g216332; PIDN:BAA01122.1; PID:g216334
A: Experimental source: strain Marburg 168T
R: Overhoff, B.; Klein, M.; Spies, M.; Friedl, R.
Mol. Gen. Genet. 228, 417-423, 1991
A: Title: Identification of a gene fragment which codes for the 364 amino-terminal and
export apparatus in gram-positive and gram-negative bacteria.
A: Reference number: S17771; MUID: 91375427
A: Accession: S17771
A: Molecule type: DNA
A: Residues: 1-125, 127-364 <OVE>
A: Cross-references: EMBL:X62035; NID:g48979; PIDN:CAA43977.1; PID:g48980
R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N. M.;
A.; Ehrlich, S. D.; Emmerson, P. T.; Entian, K. D.; Errington, J.; Fabelt, C.; Ferrari,
Nature 390, 249-256, 1997
A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
lechi, J.; Harwood, C. R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A: Authors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S. H.; Parro, V.; Pohl, T. M.; Potte
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A: Authors: Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, Y.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toynon, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A: Authors: Yoshikawa, H. F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A: Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis
A: Reference number: A69580; MUID: 98044033
A: Accession: F69704
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-841 <KUN>
A: Cross-references: GB:299122; GB:AL009126; NID:g2636029; PIDN:CAB15547.1; PID:g26360
A: Experimental source: strain 168
C: Comment: This pleiotropic protein is required for cell division, sporulation, septa
C: Comment: The "nucleotide-binding motif B" and "DEAD motif" features as annotated ar
is adjacent to the identified motif and a third conserved motif is approximately 120-1
C: Genetics:
A: Gene: secA; div
C: Superfamily: preprotein translocase secA
C: Keywords: ATP; membrane-associated complex; P-loop; protein transport; sporulation
F: 100-107/Region: nucleotide-binding motif A (P-loop) #status atypical
F: 203-208/Region: nucleotide-binding motif B
F: 207-210/Region: DEXH motif

Query Match 60.6%; Score 43; DB 2; Length 841;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 MYGVTLHEGN 12
DB 86 IMGVALLHDGN 96

RESULT 14
B48826
high choriotytic hatching proteinase (EC 3.4.24.-) HCE23 precursor - Japanese medaka
C: Species: Oryzias latipes (Japanese medaka)
C: Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C: Accession: B48826
R: Yasumasa, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shinada, H.; Yamag
Dev. Biol. 153, 250-258, 1992
A: Title: Isolation of cDNAs for ICE and HCE, two constituent proteases of the hatchin
A: Reference number: A48826; MUID: 93012471
A: Accession: B48826
A: Molecule type: mRNA; protein
A: Residues: 1-270 <YAS>
A: Cross-references: GB:M96170; NID:g213501; PIDN:AAA49438.1; PID:g213502
A: Experimental source: Orange red variety, embryo
A: Note: sequence extracted from NCBI backbone (NCBIN:114769, NCBI:114770)
C: Superfamily: astacin; astacin homology

C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-70/Domain: propeptide #status predicted <PRO>
 F:71-270/Product: low choriolytic hatching proteinase #status predicted <MAT>
 F:88-270/Domain: astacin homology <AST>
 F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:169,173,179,225/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:170/Active site: Glu #status predicted

Query Match 59.2%; Score 42; DB 2; Length 270;
 Best Local Similarity 58.3%; Pred. No. 6.7;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CMYGGVTLHEGN 12
 ||| |:
 Db 161 CMYSGIIQHLELN 172

RESULT 15

C48826 high choriolytic hatching proteinase (EC 3.4.24.-) HCE21 precursor - Japanese medaka
 C:Species: Oryzias latipes (Japanese medaka)
 C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 03-Dec-1999
 C:Accession: C48826
 R:Yasumasu, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, Dev. Biol. 153, 250-258, 1992
 A:Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching e
 A:Reference number: A48826; MUID:93012471
 A:Accession: C48826
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-279 <YAS>
 A:Cross-references: GB:M96171
 C:Superfamily: astacin; hydrolase; metalloproteinase; zinc
 C:Keywords: glycoprotein; signal sequence #status predicted <SIG>
 F:1-20/Domain: signal sequence #status predicted <PRO>
 F:21-79/Domain: propeptide #status predicted <MAT>
 F:80-279/Product: low choriolytic hatching proteinase #status predicted <MAT>
 F:97-279/Domain: astacin homology <AST>
 F:62/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:178,182,188,234/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:179/Active site: Glu #status predicted

Query Match 59.2%; Score 42; DB 2; Length 279;
 Best Local Similarity 58.3%; Pred. No. 7;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CMYGGVTLHEGN 12
 ||| |:
 Db 170 CMYSGIIQHLELN 181

Search completed: January 2, 2002, 20:49:25
 Job time: 785 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:50:15 ; Search time 37.4 Seconds
(without alignments)
11.764 Million cell updates/sec

Title: US-09-335-581A-34
Perfect score: 71

Sequence: 1 CMYGGVTLHEGN 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_39:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	90.1	266	ETC1_STAAU	P01553 staphylococ
2	64	90.1	266	ETC2_STAAU	P34071 staphylococ
3	64	90.1	266	ETC3_STAAU	P23313 staphylococ
4	62	87.3	257	ETXA_STAAU	P13163 staphylococ
5	62	87.3	257	ETXE_STAAU	P12993 staphylococ
6	60	84.5	251	SPEA_STRPY	P08095 streptococc
7	59	83.1	266	ETXB_STAAU	P01552 staphylococ
8	58	81.7	258	ETXD_STAAU	P20723 staphylococ
9	43	60.6	841	SECA_BACSU	P28366 bacillus su
10	42	59.2	270	HCE1_ORYLA	P31580 oryzias lat
11	42	59.2	279	HCE2_ORYLA	P31581 oryzias lat
12	42	59.2	895	SECA_CVACA	O13911 cyandium c
13	41.5	58.5	463	FIBB_CHICK	O02020 gallus gall
14	41	57.7	437	ERR1_YEAST	P42222 saccharomyc
15	40	56.3	810	NEL1_HUMAN	O02813 homo sapien
16	40	56.3	810	NEL1_RAT	O02919 rattus norv
17	40	56.3	904	SECA_RHOCA	P32966 rhodobacter
18	40	56.3	969	KBF1_HUMAN	P19838 homo sapien
19	40	56.3	971	KBF1_MOUSE	P25799 mus musculu
20	39	54.9	170	R57_DESMO	P41206 desulfuroc
21	39	54.9	805	PIE1_SCHPO	O09422 schistosach
22	38	53.5	413	HEMO_MANSE	P13398 manduca sex
23	38	53.5	836	SECA_LISNO	P47847 listeria mo
24	37	52.1	689	YO27_BPHPI	P51731 bacterioph
25	37	52.1	984	SECA_AOUAE	O07718 aquilex aeo
26	36	50.7	115	GUAN_HUMAN	O02747 homo sapien
27	36	50.7	128	YF75_MYCPN	P75204 mycoplasma
28	36	50.7	289	ISPE_BACSU	P37550 bacillus su
29	36	50.7	289	ISPE_BACSU	P37550 bacillus su
30	36	50.7	455	YSD1_CAEEL	P48459 caenorhabdi
31	36	50.7	857	PIF1_YEAST	P07271 saccharomyc
32	36	50.7	948	SECA_SYNP7	O53357 synecococc
33	36	50.7	1021	Y2R2_DROME	P16425 drosophila

ALIGNMENTS

34	35	49.3	139	1	YBPE_BURCE	P37336 burkholderi
35	35	49.3	149	1	YKKA_YEAST	P42949 saccharomyc
36	35	49.3	191	1	SPR6_YEAST	O01684 saccharomyc
37	35	49.3	251	1	ASTA_ASTFL	P07584 astacus flu
38	35	49.3	315	1	PHSS_DESBA	P13063 desulfovibr
39	35	49.3	352	1	THRC_BACSU	P04990 bacillus su
40	35	49.3	367	1	FTBP_ADEL15	P16847 human adeno
41	35	49.3	432	1	WISA_YEAST	P40564 saccharomyc
42	35	49.3	564	1	YKK9_YEAST	P34286 caenorhabdi
43	35	49.3	574	1	GAL2_YEAST	P13181 saccharomyc
44	35	49.3	700	1	TOP1_CAMJE	O9P127 campylobact
45	35	49.3	742	1	SVV2_RAT	O02563 rattus norv

RESULT 1
ETC1_STAAU STANDARD: PRT: 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYROGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.

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CC or send an email to license@sib-sib.ch).

CC EMBL: X05815; CA29260.1; -
DR PIR: A01816; ENSAC1.
DR PIR: S06356; S06356.
DR HSSP: P34071; 1SER2.
DR InterPro: IPR001961; Staph.Strep.toxin.
DR Pfam: PF01123; Staph.Strep.toxin.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
SO SEQUENCE 266 AA; 30546 MW; 3A7AB59AB986853B CRC64;

Query Match 90.1%; Score 64; DB 1; Length 266;
 Best Local Similarity 83.3%; Pred. No. 0.00061;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
 |||||:|||||
 DB 137 CMYGVTLHEGN 148

RESULT 2

ETC2_STAU ID ETC2_STAU STANDARD; PRT; 266 AA.
 AC P34071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
 GN ENT2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-66.
 RX MEDLINE=69277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal enterotoxins C1 and C2."
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from Staphylococcus aureus reveals a zinc-binding site."
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal enterotoxins."
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and RT dissimilarity."
 RL J. Mol. Biol. 269:270-280(1997).
 CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES PROGENIC EXOTOXINS ARE ALL RELATED.
 CC PIR; A60114; A60114.
 DR PDB; 1STE; 23-DEC-96.
 DR PDB; 1SE2; 08-MAR-96.
 DR InterPro: IPR001961; Staph.Strep.toxin.
 DR Pfam: PF01123; Staph.Strep.toxin; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; zinc; 3d-structure.
 FT SIGNAL 1 27
 FT CHAIN 1 266 ENTEROTOXIN TYPE C-2.
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 SO SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 90.1%; Score 64; DB 1; Length 266;
 Best Local Similarity 83.3%; Pred. No. 0.00061;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
 |||||:|||||
 DB 137 CMYGVTLHEGN 148

RESULT 3

ETC3_STAU ID ETC3_STAU STANDARD; PRT; 266 AA.
 AC P23313;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
 GN ENT3.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackett S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of all three type C staphylococcal enterotoxins."
 RL Mol. Gen. Genet. 220:329-333(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECP.
 RX MEDLINE=97064178; PubMed=8906797;
 RA Fields B.A., Malchiodi E.L., Li H., Yern X., Stauffer C.V.,
 RA Schlievert P.M., Karjalainen K., Marizza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a superantigen."
 RL Nature 384:188-192(1996).
 CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES PYROGENIC EXOTOXINS ARE ALL RELATED.
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 CC EMBL; X51661; CAA35972.1; -
 DR PIR; S11885; S11885.
 DR PDB; 1JCK; 12-NOV-97.
 DR InterPro: IPR001961; Staph.Strep.toxin.
 DR Pfam: PF01123; Staph.Strep.toxin; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; 3d-structure.
 FT SIGNAL 1 27
 FT CHAIN 1 266 ENTEROTOXIN TYPE C-3.
 FT DISULFID 120 137 BY SIMILARITY.
 FT CHAIN 1 266
 SO SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FFCA59 CRC64;

Query Match 90.1%; Score 64; DB 1; Length 266;
 Best Local Similarity 83.3%; Pred. No. 0.00061;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12

|||||
137 CMYGVTLHHEGN 148

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RESULT 4
ETX\STAU STANDARD; PRT; 257 AA.
ID ETX\STAU STANDARD; PRT; 257 AA.
AC P13163:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE A PRECURSOR (SEA).
GN ENTA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
  Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR1337;
RX MEDLINE=88086892; PubMed=3335483;
RA Beutley M.J.; Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
  J. Bacteriol. 170:34-41(1988).
RN [2]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
  Huang I.-Y.; Hughes J.L.; Bergdoll M.S.; Schantz E.J.;
  "Complete amino acid sequence of staphylococcal enterotoxin A.";
  J. Biol. Chem. 262:7006-7013(1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
  Sched E.M.; Zaitseva T.; Zaitsev V.N.; Dohlsten M.; Kalland T.;
  Schlievert P.M.; Ohlendorf D.H.; Svensson L.A.;
  "Crystal structure of the superantigen staphylococcal enterotoxin
  type A.";
  EMBO J. 14:3292-3301(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278;
  Sundstrom M.; Hallen D.; Svensson A.; Sched E.; Dohlsten M.;
  Abrahamson L.;
  "The Co-crystal structure of staphylococcal enterotoxin type A with
  Zn2+ at 2.7-A resolution. Implications for major histocompatibility
  complex class II binding.";
  J. Biol. Chem. 271:3212-3221(1996).
RN [5]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
  Swaminathan S.; Furey W.F. Jr.; Pletcher J.; Sax M.;
  "Residues defining V beta specificity in staphylococcal
  enterotoxins.";
  Nat. Struct. Biol. 2:680-686(1995).
RN [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070;
  Sched E.M.; Papageorgiou A.C.; Svensson L.A.; Acharya K.R.;
  "A structural and functional comparison of staphylococcal
  enterotoxins A and C2 reveals remarkable similarity and
  dissimilarity.";
  J. Mol. Biol. 269:270-280(1997).
RN [7]
RP SUBUNIT: MONOMER.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M18970; AAA26681.1; -.
DR PIR; A28664; A28664.
DR PIR; A29566; A29566.
DR PDB; 1ESF; 1JUL-96.
DR PDB; 1SEA; 15-OCT-95.
DR PDB; 1SXT; 19-NOV-97.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTERIOTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 257 ENTEROTOXIN TYPE A.
FT DISULFID 120 130
FT METAL 25 25
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T -> S (IN REF. 2).
SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCA1F14677 CRC64;

Query Match 87.38; Score 62; DB 1; Length 257;
Best Local Similarity 83.38; Pred. No. 0.0013;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHHEGN 12
Db 130 CMYGVTLHHEGN 141

RESULT 5
ETX\STAU STANDARD; PRT; 257 AA.
ID ETX\STAU STANDARD; PRT; 257 AA.
AC P12935;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN ENTE.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
  Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-74.
RC STRAIN=MJB265;
RX MEDLINE=88257005; PubMed=3384800;
  Couch J.L.; Solits M.T.; Beutley M.J.;
  "Cloning and nucleotide sequence of the type E staphylococcal
  enterotoxin gene.";
  J. Bacteriol. 170:2954-2960(1988).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
  Swaminathan S.; Furey W.F. Jr.; Pletcher J.; Sax M.;
  "Residues defining V beta specificity in staphylococcal
  enterotoxins.";
  Nat. Struct. Biol. 2:680-686(1995).
RN [3]
RP DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
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CC -----
DR EMBL; M21319; AAA26617.1; -.
DR PIR; A28179; A28179.
DR PDB; 1SEE; 15-OCT-95.
DR InterPro; IPR001961; Staph.Strep.toxin.
DR Pfam; PF01123; Staph.Strep.toxin; 1.
DR PRINTS; PR00279; BACTRLOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Eutoerotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1
FT CHAIN 28 257 ENTEROTOXIN TYPE E.
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CMC64;

Query Match
Best Local Similarity 87.3%; Score 62; DB 1; Length 257;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
Db 130 CMYGVTLHDNN 141

RESULT 6
SPEA_STRPY STANDARD; PRI; 251 AA.
ID SPEA_STRPY
AC P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE EKOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
DE (SPE A).
DE
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
ON 11
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J."
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT t12."
RT Infect. Immun. 52:144-150(1986).
RL 12
RP SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italien J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).
RN 131
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic toxin A (SpeA) by MHC class II molecules and T-cell
RT receptors."
RL EMBO J. 18:9-21(1999).
RP
CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC FEVER.
CC -2- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -3- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EKOTOXINS ARE ALL RELATED.

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CC	or send an email to license@isb-sib.ch)
DR	EMBL; U04053; AAC48868.1; -;
DR	EMBL; X03929; CAA27568.1; -;
DR	PIR; A26152; A26152.
DR	PIR; S29659; S29659.
PDB	1BIZ; 24-NOV-99.
DR	InterPro: IPR001961; Staph.Strep_toxin.
DR	pfam; PF01123; Staph_Strep_toxin.1.
DR	PRINTS; PR00279; BACTRLTOXIN.
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW	Toxin; Signal; 3D-structure.
FT	SIGNAL
FT	CHAIN 1 30
FT	DISULFID 117 128
FT	CONFLICT 6
FT	CONFLICT 17 18 K -> E (IN REF. 2).
FT	CONFLICT 25 35 VT -> MK (IN REF. 2).
FT	CONFLICT 40 40 SOEYFAQDDP -> LPEGLICSTREK (IN REF. 2).
FT	CONFLICT 43 43 H -> Q (IN REF. 2).
FT	CONFLICT 44 43 S -> N (IN REF. 2).
FT	CONFLICT 47 59 NLONTFLYEEDP -> TFKIIFPMRYTL (IN REF. 2).
FT	CONFLICT 129 129 I -> L (IN REF. 2).
FT	CONFLICT 165 178 TNKKMVAQAQLDYK -> QINGNCSRIYST (IN REF. 2).
SQ	SEQUENCE 251 AA; 29246 MW; 54001FEACCBFC3 CRC64;
OY	1 CMYGVTLEHGN 12
Dd	128 CIYGVTVNHGN 139
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Matches	10; Conservative 83.3%; Pred. No. 0.0028; Mismatches 1; Indels 0; Gaps 0;
RESULT 7	
ID	ETXB_STAUV STANDARD; PRT; 266 AA.
AC	P01552;
DT	21-JUL-1986 (Rel. 01, Created)
DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	ENTEROTOXIN TYPE B PRECURSOR (SEB).
GN	ENTB.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OC	Bacillus/Staphylococcus group; Staphylococcus.
OX	NCBI_Taxid=1280;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=86168029; PubMed=3957869;
RT	Jones C.L., Khan S.A.;
RT	"Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT	aureus".
RL	J. Bacteriol. 166:29-33(1986).
RN	[2]
RP	SEQUENCE OF 40-91 FROM N.A.
RA	MEDLINE=85298255; PubMed=3898073;
RA	Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT	"Molecular cloning of staphylococcal enterotoxin B gene in
RT	Escherichia coli and Staphylococcus aureus".
RT	Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN	[3]

```

RX SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence.";
RL J. Biol. Chem. 245:3518-3525(1970).
RN
RN
RN
RN
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483;
RA Jaderczyk T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RA Chl Y.I., Staufferacher C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RL Nature 368:711-718(1994).
RN
RN
RN
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=99096298; PubMed=9881971;
RA Li H., Liere A., Tsuchiya D., Leder L., Ysern X., Schliwert P.M.,
RA Katjalainen K., Maritzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN
RN
RN
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 227:61-79(1998).
CC
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC
CC
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CC
DR EMBL; M11118; AAA88550.1; -.
DR PIR; A01815; ENSAB6.
DR PIR; S27360; S27360.
DR PDB; 1SEB; 20-JUN-96.
DR PDB; 2SEB; 28-JAN-96.
DR PDB; 3SEB; 27-MAY-98.
DR PDB; 1SE4; 16-JUN-97.
DR PDB; 1SE4; 15-OCT-97.
DR PDB; 1SB8; 04-MAR-99.
DR InterPro; IPR001961; Staph.Strep.toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL
FT CHAIN
FT 1 27
FT 28 266 ENTEROTOXIN TYPE B.
FT DISULFID
FT 120 140
FT CONFLICT
FT 56 58 DON -> NND (IN REF. 3).
FT CONFLICT
FT 69 77 DQFLYFDL -> NEFFLYL (IN REF. 3).
FT CONFLICT
FT 118 118 MISSING (IN REF. 3).
FT CONFLICT
FT 128 130 DIN -> NID (IN REF. 3).
FT CONFLICT
FT 133 135 QTD -> ENT (IN REF. 3).

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Query Match	Best Local Similarity	83.1%	Score 59	DB 1	Length 266			
Matches 10	Conservative	0	Mismatches	2	Indels	0	Gaps	0
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Db	140 CMYGVTEHNGN 151							
RESULT 8								
ID	ETXD_STAAU	STANDARD	PRT	258 AA				
AC	P20723							
DT	01-FEB-1991 (Rel. 17, Created)							
DT	01-FEB-1991 (Rel. 17, Last sequence update)							
DT	15-JUL-1999 (Rel. 38, Last annotation update)							
DE	ENTEROTOXIN TYPE D PRECURSOR (SED).							
GN	ENTD.							
OS	Staphylococcus aureus.							
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;							
OC	Bacillus/Staphylococcus group; Staphylococcus.							
OX	NCBI_TaxID=1280;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE=89359112; PubMed=2549000;							
RA	Bayles K.W., Iandolo J.J.;							
RT	"Genetic and molecular analyses of the gene encoding staphylococcal							
RL	enterotoxin D.";							
	J. Bacteriol. 171:4799-4806(1989).							
RN	[2]							
RP	SEQUENCE FROM N.A. AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).							
RC	STRAIN=ATCC 23235;							
RX	MEDLINE=97157473; PubMed=9003758;							
RA	Sundstroem M., Abrahamsen L., Antonsson P., Melnate K., Mourad W.,							
RT	Dohlsten M.;							
RL	"The crystal structure of staphylococcal enterotoxin type D reveals							
CC	zn2+-mediated homodimerization.";							
CC	EMBO J. 15:6832-6840(1996).							
CC	-1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.							
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION							
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.							
CC	-1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES							
CC	PYROGENIC EXOTOXINS ARE ALL RELATED.							
CC	-----							
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CC	-----							
DR	EMBL; M28521; AAB06195.1; -.							
DR	PIR; A33953; A33953.							
DR	HSSP; P13163; 1SXT.							
DR	InterPro: IPR001961; Staph.strep.toxin.							
DR	Pfam: PF01123; Staph.strep.toxin.1.							
DR	PRINTS; PR00279; BACTR1TOXIN.							
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.							
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.							
KW	Enterotoxin; Toxin; Signal; Supercatigen; Zinc.							
FT	SIGNAL 1 25							
FT	CHAIN 26 258							
FT	METAL 212 212							
FT	METAL 250 250							
	ZINC.							
	ZINC.							
	ENTEROTOXIN TYPE D.							
	ZINC.							
	ZINC.							

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FT METAL 252 252 ZINC.
FT VARIANT 114 114 P->A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 4E7C6A28D42597ED.CRC64;

Query Match
Best Local Similarity 81.7%; Score 58; DB 1; Length 258;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
   1 11111 1111
Db 131 CTYGGVTPHEGN 142

RESULT 9
SECA_BACSU STANDARD; PRT; 841 AA.
AC P28366;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.
GN SECA OR Div+.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / MARBURG;
RX MEDLINE=91192600; PubMed=1901557;
RA Sadale Y., Takamatsu H., Nakamura K., Yamane K.;
RT "Sequencing reveals similarity of the wild-type div+ gene of Bacillus
   subtilis to the Escherichia coli seca gene."
RL Gene 98:101-105(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX Soldo B., Lazarevic V., Manuel C., Karamata D.;
RL submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-364 FROM N.A.
RC STRAIN-ATCC 6057;
RX MEDLINE=91375427; PubMed=1832735;
RA Overhoff B., Klein M., Spies M., Freudl R.;
RT "Identification of a gene fragment which codes for the 364 amino-
   terminal amino acid residues of a SecA homologue from Bacillus
   subtilis: further evidence for the conservation of the protein export
   apparatus in gram-positive and gram-negative bacteria."
RL Mol. Gen. Genet. 228:417-423(1991).
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SECE
   SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF
   ATP TO THE TRANSFER OF PRE-SECRETORY PERIPLASMIC AND OUTER
   MEMBRANE PROTEINS ACROSS THE MEMBRANE.
CC -1- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
   WHICH COMPRISE SECA, SECB, SECD, SECE, SECF, SECG AND SECY
   (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MEMBRANE, AND
   CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D10279; BAA01122.1; -
CC EMBL: U56901; AAC44957.1; -
CC EMBL: X62035; CAA43977.1; -
CC EMBL: Z99122; CAB15547.1; -

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DR PIR: J00647; J00647.
DR PIR: S17771; S17771.
DR Subtilisin; BG10741; seca.
DR InterPro: IPR000185; seca.
DR Pfam: PF01043; SecA_protein; 1.
DR PRINTS: PR00906; SECA.
DR PROSITE: PS01312; SECA; 1.
KW protein transport; ATP-binding; Membrane; Translocation; Transport;
KM Complete proteome.
FT NP_BIND 100 107 ATP (POTENTIAL).
FT CONFLICT 126 126 V->I (IN REF. 3).
SQ SEQUENCE 841 AA; 95530 MW; 9AAC3630139F5EEF.CRC64;

Query Match
Best Local Similarity 60.6%; Score 43; DB 1; Length 841;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 MYGCVTLHEGN 12
   1 11 1111
Db 86 LMGSVALHDSN 96

RESULT 10
HCEL_ORYLA STANDARD; PRT; 270 AA.
ID HCEL_ORYLA
AC P31580;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HIGH CHORIOLYTIC ENZYME 1 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME
   ZINC-PROTEINASE HCE 1 SUBUNIT) (CHORIOLYSIN H 1).
GN HCE 23.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 71-119 AND 208-223.
RC TISSUE=embryo;
RX MEDLINE=93012471; PubMed=1397682;
RA Yasunasu S., Yamada K., Akasaka K., Mitsuana K., Iuchi I.,
RA Shimada H., Yamagami K.;
RT "Isolation of cDNAs for ICE and HCE, two constituent proteases of the
   hatching enzyme of Oryzias latipes, and concurrent expression of
   their mRNAs during development."
RL Dev. Biol. 153:250-258(1992).
CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,
   WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME
   OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.
CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE
   CHORIOLYTIC SMELLING ACTION.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG
   ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES
   SUCH AS SUC-LEU-LEU-VAL-TYR-I-MCA.
CC -1- COFACTOR: BINDS ONE ZINC ION.
CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZMOGEN
   GRANULES.
CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY
   2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.
CC -1- PTM: O-GLYCOSYLATED (PROBABLE).
CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF
   TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE), OF
   WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME
   (LCE).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
   METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
CC -----
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CC EMBL: M96170; AAA49438.1; -
 DR PIR: B48826; B48826.
 DR HSSP: P07584; 1IAD.
 DR MEROPS: M12.007; -
 DR InterPro: IPR001506; Astacin.
 DR InterPro: IPR000130; Zn_Mtpeptidase.
 DR Pfam: PF01400; Astacin.1.
 DR PRINTS: PRO0480; ASTACIN.
 DR SMART: SM00235; zmc; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Hydroxylase; Metalloprotease; zinc; Glycoprotein; zymogen; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 70 ACTIVATION PEPTIDE.
 FT CHAIN 71 270 HIGH CHORIOLYTIC ENZYME 1.
 FT METAL 169 169 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 170 170 BY SIMILARITY.
 FT METAL 173 173 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 179 179 ZINC (CATALYTIC) (BY SIMILARITY).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 270 AA; 30392 MW; D85C9729063735A CRC64;

Query Match 59.2%; Score 42; DB 1; Length 270;
 Best Local Similarity 58.3%; Pred. No. 3.8;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
 DB 161 CMYSGTIQHELN 172

RESULT 11
 HCE2_ORYLA STANDARD; PRT; 279 AA.
 AC P1361;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HIGH CHORIOLYTIC ENZYME 2 PRECURSOR (EC 3.4.24.67) (HATCHING ENZYME
 DE ZINC-PROTEASE HCE 2 SUBUNIT) (CHORIOLYSIN H 2).
 GN HCE 21.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adiantichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=93012471; Pubmed=1397682;
 RA Vesunasu S., Yamada K., Akasaka K., Mitsunaga K., Iuchi I.,
 RA Shimada H., Yamagami K.;
 RT Isolation of cDNAs for LCE and HCE, two constituent proteases of the
 RT hatching enzyme of Oryzias latipes, and concurrent expression of
 RT their mRNAs during development.*;
 RL Dev. Biol. 153:250-258(1992).
 CC -1- FUNCTION: PARTICIPATES IN THE BREAKDOWN OF THE EGG ENVELOPE,
 CC WHICH IS DERIVED FROM THE EGG EXTRACELLULAR MATRIX, AT THE TIME
 CC OF HATCHING. THUS ALLOWING THE NEWLY HATCHED FISH TO SWIM FREE.
 CC HCE BINDS TIGHTLY TO THE EGG ENVELOPE WHILE IT EXERTS THE
 CC CHORIOLYTIC SMELLING ACTION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE INNER LAYER OF FISH EGG
 CC ENVELOPE. ALSO HYDROLYSES CASEIN AND SMALL MOLECULE SUBSTRATES
 CC SUCH AS SUC-LEU-LEU-TYR-I-MCA.
 CC -1- COFACTOR: BINDS ONE ZINC ION.
 CC -1- SUBCELLULAR LOCATION: STORED AS PROENZYMES IN THE ZYMOGEN
 CC GRANULES.

CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF THE PROTEIN STARTS IN DAY
 CC 2 TO DAY 3 EMBRYOS AND INCREASES THEREAFTER UNTIL HATCHING.
 CC -1- PM: O-GLYCOSYLATED (PROBABLE).
 CC -1- MISCELLANEOUS: IN MEDAKA THE HATCHING ENZYME SYSTEM IS COMPOSED OF
 CC TWO DISTINCT PROTEASES, THE HIGH CHORIOLYTIC ENZYME (HCE), OF
 CC WHICH THERE ARE TWO ISOFORMS, AND THE LOW CHORIOLYTIC ENZYME
 CC (LCE).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
 CC METALLOPROTEASE); ALSO KNOWN AS THE ASPRACIN SUBFAMILY.
 CC
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CC EMBL: M96171; AAA49439.1; -
 DR HSSP: P07584; 1IAD.
 DR MEROPS: M12.007; -
 DR InterPro: IPR001506; Astacin.
 DR InterPro: IPR000130; Zn_Mtpeptidase.
 DR Pfam: PF01400; Astacin.1.
 DR PRINTS: PRO0480; ASTACIN.
 DR SMART: SM00235; zmc; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Hydroxylase; Metalloprotease; zinc; Glycoprotein; zymogen; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 79 ACTIVATION PEPTIDE.
 FT CHAIN 80 279 HIGH CHORIOLYTIC ENZYME 2.
 FT METAL 178 178 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 179 179 BY SIMILARITY.
 FT METAL 182 182 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 188 188 ZINC (CATALYTIC) (BY SIMILARITY).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 279 AA; 31490 MW; 00244107A8B01B8C CRC64;

Query Match 59.2%; Score 42; DB 1; Length 279;
 Best Local Similarity 58.3%; Pred. No. 3.9;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CMYGVTLHEGN 12
 DB 170 CMYSGTIQHELN 181

RESULT 12
 SECA_CYACA STANDARD; PRT; 895 AA.
 AC O19911;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PREPROTEIN TRANSLOCASE SECA SUBUNIT.
 GN SECA.
 OS Cyanidium caldarium.
 OS Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
 OC Cyanidium.
 OX NCBI_TaxID=2771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RK-1;
 RX MEDLINE=20496959; Pubmed=11040290;
 RA Gloeckner G., Rosenthal A., Valentin K.;
 RT The structure and gene repertoire of an ancient red algal plastid
 RT genome.*;
 RL J. Mol. Evol. 51:382-390(2000).
 CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT AND IMPORT. SECA HAS A
 CC CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF ATP TO THE TRANSFER OF
 CC PRE-SECRETORY PROTEINS ACROSS THE MEMBRANE.

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF02186; AAB82678.1; -.
 CC InterPro: IPR000185; SecA.
 CC Pfam: PF01043; SecA_protein; 1.
 CC PRINTS: PR00906; SECA.
 CC PROSITE: PS01312; SECA; 1.
 CC Protein transport; ATP-binding; Chloroplast; Translocation; Transport.
 CC NP_BIND 105 112 ATP (BY SIMILARITY).
 CC SEQUENCE 895 AA; 103753 MW; DB290CFD201EADBC CRC64;
 SQ
 Query Match 59.2%; Score 42; DB 1; Length 895;
 Best Local Similarity 70.0%; Pred. No. 12;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 2 MYGGVTLHEG 11
 DB 91 MGGIVLHEG 100
 RESULT 13
 FIBB.CHICK STANDARD; PRT; 463 AA.
 AC 002020:
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FIBRINOGEN BETA CHAIN PRECURSOR (FRAGMENT).
 GN FGB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 [1]
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
 MEDLINE=91182745; PubMed=2009286;
 RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
 RT "The beta chain of chicken fibrinogen contains an atypical thrombin
 RT cleavage site";
 RT Biochemistry 30:3290-3294(1991).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC -----
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 CC -----

CC EMBL: M58514; AAA48770.1; -.
 CC PIR: A38463; A38463.
 CC HSSP: P02675; 1FZB.
 CC InterPro: IPR002181; Fibrinogen_C.
 CC Pfam: PF00147; fibrinogen_C; 1.
 CC SMART: SM00186; FGB; 1.
 CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 CC KW: blood coagulation; plasma; platelet; glycoprotein; sulfation.
 CC FT NON_TER 1 1
 CC FT PEPTIDE <1 17 FIBRINOPEPTIDE B.
 CC FT CHAIN 18 463 FIBRINOGEN BETA CHAIN.
 CC FT MOD_RES 5 5 SULFATION (BY SIMILARITY).
 CC FT SITE 17 18 CLEAVAGE (BY THROMBIN: RELEASE
 CC FT FIBRINOPEPTIDE B).
 CC FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
 CC FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
 CC FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
 CC FT DISULFID 197 197 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
 CC FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
 CC FT DISULFID 205 289 BY SIMILARITY.
 CC FT DISULFID 215 244 BY SIMILARITY.
 CC FT DISULFID 397 410 BY SIMILARITY.
 CC FT CARBOHYD 367 367 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 463 AA; 52678 MW; 2044CD49BA9EC7B CRC64;
 SQ
 Query Match 58.5%; Score 41.5; DB 1; Length 463;
 Best Local Similarity 66.7%; Pred. No. 7.6;
 Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 OY 2 MYGGVTLH-BGN 12
 DB 328 LYGFTTHNEGN 339
 RESULT 14
 ERL1.YEAST STANDARD; PRT; 437 AA.
 ID ERL1.YEAST
 AC P42222:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ENOLASE RELATED PROTEIN 1 (EC 4.2.1.11).
 DE ENOLASE RELATED PROTEIN 1 (EC 4.2.1.11).
 GN ERL1 OR YMR323W OR YMR924.15.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=S288C / AB972;
 RC Churcher C.N., Louis E.J., Barrall B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE OF 120-437 FROM N.A.
 RC STRAIN=S288C / YPI;
 RX MEDLINE=95304851; PubMed=7765338;
 RA Pryde F.E., Huckle T.C., Louis E.J.;
 RT "Sequence analysis of the right end of chromosome XV in Saccharomyces
 RT cerevisiae: an insight into the structural and functional
 RT significance of sub-telomeric repeat sequences";
 RT Yeast 11:371-382(1995).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; Z54141; CAAG0841.1; -.
DR EMBL; UZ3472; AAC48992.1; -.
DR HSSP; P00924; INEL.
DR SGD; S0005920; ERRI.
DR InterPro; IPR000941; Enolase.
DR pfam; PF00113; enolase; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium.
FT ACT_SITE 160 160 BY SIMILARITY
FT METAL 246 247 MAGNESIUM (BY SIMILARITY)
FT METAL 296 296 MAGNESIUM (BY SIMILARITY)
FT METAL 321 321 MAGNESIUM (BY SIMILARITY)
SQ SEQUENCE 437 AA; 47312 MW; 143DBEF6FBD3D13 CRC64;

OY 1 CMYGGVTLHECN 12
DB 424 CIVAGHREFHGN 435

RESULT 15
ID NEEL_HUMAN STANDARD: PRT; 810 AA.
AC Q92832; Q9Y472;
DT 01-NOV-1997 (Rel. 35, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTEIN KINASE C-BINDING PROTEIN NELL1 PRECURSOR (NEL-LIKE PROTEIN 1)
DE (NEL-RELATED PROTEIN 1).
GN NELL1 OR NRPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91131504; PubMed=8975702;
RA Maranbe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
RT Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.,
RT "Cloning and characterization of two novel human CDKnas (NELL1 and
RL NELL2) encoding proteins with six EGF-like repeats.";
RN RL Genomics 38:273-276(1996).
[2]
RP SEQUENCE OF 383-810 FROM N.A.
RA Ting K., Vascardis H., Mulliken J.B., Bertolami C., Wen Z.,
RA Young M., Tieu A., Kwong E.;
RL "Nel homolog gene expression in craniofacial anomalies.";
RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
CC -1-SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
CC -1-SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -1-DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.
CC -1-SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.
CC -1-SIMILARITY: CONTAINS 5 WWC DOMAINS.
CC -1-SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC -1-CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
CC IN POSITIONS 427 AND 771.
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[illegible]

Query Match 56.3%; Score 40; DB 1; Length 810;
Best Local Similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CMYGSVTLHEG 11
I:|I| I|I
Db 335 CIYGKVIAGE 345

Search completed: January 2, 2002, 20:50:16
Job time: 211 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 2, 2002, 20:52:02 ; Search time 92.66 Seconds
(Without alignments)
18.943 Million cell updates/sec

Title: US-09-335-581A-34
Perfect score: 71
Sequence: 1 CMYGGVTLHEGN 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.podent:*
13: sp.virus:*
14: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	65	90.1	268	2	085217	085217 staphylococ
2	64	90.1	234	2	09R5X4	09R5X4 staphylococ
3	64	90.1	239	2	005157	005157 staphylococ
4	64	90.1	239	2	053678	053678 staphylococ
5	64	90.1	239	2	006531	006531 staphylococ
6	64	90.1	239	2	006532	006532 staphylococ
7	64	90.1	239	2	006533	006533 staphylococ
8	64	90.1	239	2	006534	006534 staphylococ
9	64	90.1	239	2	006535	006535 staphylococ
10	64	90.1	271	2	09F0L6	09F0L6 staphylococ
11	63	88.7	258	2	09EZM4	09EZM4 staphylococ
12	62	87.3	260	2	099SU3	099SU3 staphylococ
13	61	85.9	136	2	099T49	099T49 staphylococ
14	60	84.5	222	2	09S5Z4	09S5Z4 streptococ
15	60	84.5	222	2	09R9J1	09R9J1 streptococ
16	60	84.5	236	2	054696	054696 streptococ
17	60	84.5	236	2	054779	054779 streptococ
18	60	84.5	236	2	057453	057453 streptococ
19	60	84.5	236	2	P97163	P97163 streptococ

20	58	81.7	179	2	052075	052075 plasmid p1b
21	52	73.2	260	2	099T46	099T46 staphylococ
22	52	73.2	261	2	09EZM8	09EZM8 staphylococ
23	51	71.8	260	2	054738	054738 streptococ
24	51	71.8	260	2	054971	054971 streptococ
25	51	71.8	260	2	054739	054739 streptococ
26	47	66.2	157	2	099RP7	099RP7 staphylococ
27	44	62.0	225	2	091921	091921 streptococ
28	44	62.0	225	2	099ZJ1	099ZJ1 streptococ
29	42	59.2	266	13	013116	013116 oryzae lat
30	41	57.7	335	2	09A5S5	09A5S5 caulobacter
31	41	57.7	347	4	09NML4	09NML4 homo saplen
32	41	57.7	437	3	012007	012007 saccharomyc
33	41	57.7	1266	4	09NVE6	09NVE6 homo saplen
34	41	57.7	1353	4	09B1E8	09B1E8 homo saplen
35	40	56.3	241	2	053585	053585 staphylococ
36	40	56.3	258	2	092N22	092N22 staphylococ
37	40	56.3	258	2	09EZM3	09EZM3 staphylococ
38	40	56.3	258	2	085382	085382 staphylococ
39	40	56.3	968	4	09NZC0	09NZC0 homo saplen
40	39	54.9	63	2	09EM93	09EM93 streptomyc
41	39	54.9	156	2	09JWR7	09JWR7 bacillus ha
42	42	54.9	270	2	066049	066049 enterobacte
43	39	54.9	593	2	044099	044099 anaplasma m
44	39	54.9	622	2	09APG5	09APG5 anaplasma m
45	39	54.9	623	2	09APG7	09APG7 anaplasma m

ALIGNMENTS

RESULT 1
085217 ID 085217 PRELIMINARY; PRT: 268 AA.
AC 085217;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN J.
GN SEJ.
OS Staphylococcus aureus.
OC Bacteriia; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
CX NCBI_TaxID=1280;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=KSI1410;
RC Zhang S., Iandolo J.J., Stewart G.C.;
RA "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
RT enterotoxin determinant (sej).";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053140; AAC78590.1; -.
DR HSSP; P13163; IESF.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; I.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;

Query Match 91.5%; Score 65; DB 2; Length 268;
Best Local Similarity 91.7%; Pred. No. 0.00061;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
Db 130 CMYGGVTLHEGN 141
RESULT 2

Q9R5X4
ID Q9R5X4 PRELIMINARY; PRT: 234 AA.
AC Q9R5X4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN-PYROGENIC TOXIN.
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group.
OX NCBI_TaxID=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP: P34071; ISE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 234 AA: 27122 MW: D6A7B45FB9810052 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 234;
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
Db 105 CMYGGITKHEGN 116
|||||:||||
RESULT 3
ID 005157 PRELIMINARY; PRT: 239 AA.
AC 005157;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE C ENTEROTOXIN (FRAGMENT).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U91526; AAB50248.1; -.
DR HSSP: P23313; IJCK.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA: 27536 MW: D6606446DDE4191 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
Db 110 CMYGGITKHEGN 121
|||||:||||

RESULT 4

O53678
ID O53678 PRELIMINARY; PRT: 239 AA.
AC O53678;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).
DR EMBL: L13376; AAA26620.1; -.
DR HSSP: P34071; ISE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin.
FT NON_TER 1
SQ SEQUENCE 239 AA: 27618 MW: A13E7EB25C6989C2 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CMYGGVTLHEGN 12
Db 110 CMYGGITKHEGN 121
|||||:||||
RESULT 5
ID 006531 PRELIMINARY; PRT: 239 AA.
AC 006531;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=4446;
RA MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13374; AAA26618.1; -.
DR HSSP: P34071; ISE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Supernatigen.
FT NON_TER 1
SQ SEQUENCE 239 AA: 27612 MW: BB7BD6204731ED24 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
|||||:|||||
Db 110 CMYGGITKHEGN 121

RESULT 6
ID 006532 PRELIMINARY; PRT; 239 AA.
AC 006533;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; Pubmed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13375; AAA26619.1; -
DR HSSP: P34071; 1SE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
|||||:|||||
Db 110 CMYGGITKHEGN 121

RESULT 7
ID 006533 PRELIMINARY; PRT; 239 AA.
AC 006533;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCOPELAND;
RX MEDLINE=94011313; Pubmed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;

RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13378; AAA26622.1; -
DR HSSP: P34071; 1STE.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
|||||:|||||
Db 110 CMYGGITKHEGN 121

RESULT 8
ID 006534 PRELIMINARY; PRT; 239 AA.
AC 006534;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; Pubmed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13379; AAA26623.1; -
DR HSSP: P34071; 1SE2.
DR InterPro: IPR001961; Staph_Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
|||||:|||||
Db 110 CMYGGITKHEGN 121

RESULT 9

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006535 ID 006535 PRELIMINARY; PRT; 239 AA.
AC 006535;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRI 909;
RC MEDLINE=94011313; PubMed=8406814;
RX Mart J.C., Lyon J.D., Roberson J.R., Luppert M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications."
RL Infect. Immun. 61:4234-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
CC EMBL; L33377; AAA26621.1; -.
DR HSSP; P23313; 1JCK.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E4119E0 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 0.00081;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
Db 110 CMYGVTLHEGN 121

RESULT 10
Q9F0L6 PRELIMINARY; PRT; 271 AA.
AC 09F0L6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-JUN-2001 (Tremblrel. 16, Last sequence update)
DE STAPHYLOCOCCAL ENTEROTOXIN C-BOVINE.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20566668; PubMed=11114901;
RX Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
Staphylococcus aureus encoding multiple superantigens."
RL EMBL; AF217235; AAG29599.1; -.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 90.1%; Score 64; DB 2; Length 271;

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Best Local Similarity 83.3%; Pred. No. 0.00094;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
Db 142 CMYGVTLHEGN 153

RESULT 11
Q9EZM4 PRELIMINARY; PRT; 258 AA.
AC 09EZM4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SEK (ENTEROTOXIN SEN).
GN SEK OR SEN OR SAI643.
OS Staphylococcus aureus.
OS Staphylococcus aureus subsp. aureus N315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN-A900322;
RX MEDLINE=20571956; PubMed=11123352;
RX Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
nursery of superantigens in Staphylococcus aureus."
RL J. Immunol. 166:669-677(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus subsp. aureus N315;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AF285760; AAG36956.1; -.
DR EMBL; AP003135; BAB42911.1; -.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 88.7%; Score 63; DB 2; Length 258;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
Db 133 CMYGVTLHEGN 144

RESULT 12
Q99SU3 PRELIMINARY; PRT; 260 AA.
AC 099SU3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ENTEROTOXIN P.
GN SEP OR SAI761.
OS Staphylococcus aureus subsp. aureus N315.

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OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Iian J., Ito T., Kanamori M.,
RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kunara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003135; BAB43036.1; -.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 87.3%; Score 62; DB 2; Length 260;
Best Local Similarity 83.3%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
DB 133 CMYGVTLHDNN 144
|||||||:|

RESULT 13
ID 099749 PRELIMINARY; PRT; 136 AA.
AC 099749:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE ENTEROTOXIN YENT2.
DE YENT2 OR SA1644.
OS Staphylococcus aureus subsp. aureus N315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Iian J., Ito T., Kanamori M.,
RA Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kunara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003135; BAB42912.1; -.
KW Complete proteome.
SQ SEQUENCE 136 AA; 15945 MW; D7CB619820C45FE CRC64;

Query Match 85.9%; Score 61; DB 2; Length 136;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
DB 5 CMYGVTEHDGN 16
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RESULT 14
ID 09S524 PRELIMINARY; PRT; 222 AA.
AC 09S524:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
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DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EXOTOXIN TYPE A (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Bessen D.E., Izso M.W., Fiorentino T.R., Carlingal R.M., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029051; AAD1315.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 84.5%; Score 60; DB 2; Length 222;
Best Local Similarity 83.3%; Pred. No. 0.004;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CMYGVTLHEGN 12
DB 108 CMYGVTLHEGN 119
|||||||:|

RESULT 15
ID 09R931 PRELIMINARY; PRT; 222 AA.
AC 09R931:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EXOTOXIN A (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Bessen D.E., Izso M.W., Fiorentino T.R., Carlingal R.M., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF055698; AAD11624.1; -.
DR HSSP; P08095; 1B1Z.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;
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QY 1 CMYGVTLHEGN 12
|:|||||
Db 108 CXYGVTLHEGN 119

Search completed: January 2, 2002, 20:52:02
Job time: 227 sec